

S/PB

CRYSTAL OF RIBOSOMAL RECYCLING FACTOR (RRF) PROTEIN AND APPLICATION  
THEREOF ON THE BASIS OF THREE-DIMENSIONAL STRUCTURAL DATA OBTAINED  
FROM THE CRYSTAL

Crystal

## [TECHNICAL FIELD]

The present invention relates to a crystal of ribosomal recycling factor (hereinafter referred to as RRF). The present invention also relates to the steric structure of the RRF protein obtained by X-ray diffraction of the crystal. Further, the present invention relates to the determination of the structure of RRF mutants, homologues and so forth and technology for the development of bactericides, fungicides and herbicides of next generation by application of the RRF protein on the basis of the structural data and mechanism action of the RRF protein.

## [BACKGROUND ART]

Protein biosynthesis is a function indispensable for the biological activities of all cells and consists of four steps, i.e., "initiation", "extension", "termination" and "ribosome recycling". The final step in the protein biosynthesis (the fourth step) terminates with the release and dissociation of a termination complex composed of messenger RNA, transfer RNA and ribosome individually in order for the ribosome to be recycled in the next "initiation" step. In Escherichia coli, which is a procaryote, it is known that

the ribosomal "recycling" is catalyzed by a ribosome recycling factor (hereinafter referred to as RRF), and an elongation factor G (hereinafter referred to as EFG), or a release factor 3. The process of the ribosomal "recycling" is introduced in the general remarks by Dr. Janosi et al. (1996 *Adv. Biophys.* 32:121-201) and the general remarks by Kaji et al. (*Biochem., Biophys., Res Commun.*, 250 1-4, *Protein, Nucleic Acid and Enzyme*, Vol. 44, No. 7, 83-84 (1999)).

Since the possibility that in eucaryotes, the dissociation of a protein translation termination complex is catalyzed by a factor other than RRF is suggested and since the mRNA of eucaryotes is monocistronic whereas that of prokaryotes is polycistronic (Kozak 1987, *Mol. Cell Biol.* 7:3438-3445; Das et al 1984, *Nucleic Acids Res.* 12:4757-4768; Schoner et al. 1986 *Proc. Natl. Acad. Sci. U.S.A.* 83:8506-8510; Sprengel et al. 1985 *Nucleic Acids Res.* 13:893-909), in eucaryotes, even if the dissociation of ribosome from mRNA is inhibited, this does not influence the downstream cistron. Thus, the fourth step, that is, the dissociation of protein translation termination complex, that corresponds to the final step of protein biosynthesis in eucaryotes is considered to be different from that in prokaryotes and hence there is an expectation as a target of especially a new type of antibiotic.

On the other hand, presently a large number of antibacterial agents have been developed and among them there are those that exhibit very high bactericidal effect. However, the antibacterial agents

thus obtained include a lot of whose site of action remain unclear. Thus far, the development has centered on a method in which those antibacterial agents that exhibit activity are used as a material for random screening and while establishing a structure-activity relationship the one having a further utility is being developed. However, this requires an immensity of time and labor.

Accordingly, in recent years, formation of database is being attempted with a view to eliminating this problem and efficiently finding an inhibitor. On the basis of it, a rational drug design method is being studied and developed. An example of this includes an inhibitor of protease, which is an anti-HIV agent, recently put into market. The protease of HIV has been crystallized and its protein structure has been known. On the basis of the structure and three-dimensional structural amino acid sequence of the active site, one having the highest affinity for this site has been selected from known compounds by use of a computer and its inhibitory activity has been measured. By making a eutectic between the one having activity and the target protein and performing measurement of a three-dimensional structure, an anticipation of a compound that binds better can be made and hence, this is synthesized and its inhibitory activity is measured. Then, by making a eutectic between this substance and the target protein again and repeating the above-mentioned process, an extremely effective substance can be obtained.

Note that a large number of strains that have acquired a resistance to the conventional antibiotics as described above have been reported and a quick development of a novel antibiotic targeting the site that can directly control the growth of bacteria is needed. Accordingly, the present inventors have paid attention to the possibility that the above-mentioned RRF can be a new target of bactericides and advanced their study extensively. This idea has been being in the limelight.

[DISCLOSURE OF THE INVENTION]

Concerning RRF, the present inventors have thus far identified several kinds of gene sequences with regards to beginning with Escherichia coli, not only procaryotes but also eucaryotes (Japanese Patent Application Laid-open No. Hei 3-200797, PCT/JP98/00734, Japanese Patent Application No. Hei 10-150493). Therefore, up to secondary structures can be presumed from the amino acid sequences obtained therefrom. However, in the present state of the art, it has not reached that the actual protein structure can be identified from the secondary structures. In an actual protein, respective amino acid residues mutually act and undergo various modifications as the case may be to form its protein structure. Therefore, once the steric structure of a protein is discovered, it is possible to create a substance that can serve as a ligand thereof and in this sense, in order to create a useful antibiotic, the determination

of three-dimensional structure by crystallization will have an extremely important significance.

Therefore, an object of the present invention is to clarify the steric structure of RRF and contribute to the development of various antibacterial agents, antifungal agents and herbicides.

[BRIEF DESCRIPTION OF THE DRAWINGS]

[Fig. 1] is a photograph showing an XRRF protein crystal.

[Fig. 2] is a photograph showing an X-ray diffraction pattern of an XRRF protein crystal.

Details of diffraction pattern: xf1 to 1200 of 1200, yf 1 to 1200 of 1200

Direction of diffraction pattern: xf to the right, yf up

File order of data: -xf + yf

Maximum pixel value: 65535

Limit of scale: minimum = 1, maximum = 1,200, black indicates high value of diffraction intensity.

[Fig. 3] is a photograph showing of rendering by a ribbon of RRF. As shown in the drawing, it consists of two domains, one consisting of three helices and the second domain being a complex of a  $\beta$ -sheet and a coil helix.

[Fig. 4] is a photograph of a space-packing model of RRF.

[Fig. 5] is a schematic explanatory drawing showing a hypothesis on the function mechanism of RRF.

[Fig. 6] is a graph showing that the release of transfer RNA from a termination complex is inhibited by various inhibitors. The error bar indicates standard deviation.

[Fig. 7] is a graph by Lineweaver-Burk plot showing inhibition of ribosome release in the presence of a varied concentration of transfer RNA.

[Fig. 8] is a graph showing binding of RRF to ribosome is inhibited in the presence of paromomycin. The error bar indicates standard deviation.

[DESCRIPTION OF REFERENCE NUMERALS]

1...Ribosome, 2...transfer RNA, 3...messenger RNA, 4...RRF,  
5...EFG, 6...termination complex.

In consideration of the present status as described above, the present inventors have advanced study on RRF, during which they have been successful in obtaining a crystal of RRF and identifying its steric structure for the first time. They have further advanced the study and, as a result, completed the present invention.

Therefore, the present invention relates to an RRF protein crystal, a method of preparing thereof and a steric structure.

More specifically, the present invention relates to the method for designing a compound capable of binding to an active site or an accessory binding site of an RRF protein which comprises computationally evaluating a chemical entity of the RRF protein

on the basis of a structure coordinate obtained from an RRF protein crystal.

Also, the present invention relates to the method in which the RRF protein crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

Also, the present invention relates to the method in which the RRF protein crystal is bipyramidal.

Further, the present invention relates to the method in which the RRF protein crystal has a space group P4<sub>1</sub>2<sub>1</sub>2<sub>1</sub> or a space group P4<sub>3</sub>2<sub>1</sub>2.

Also, the present invention relates to the method in which the RRF protein crystal has a size of 0.3 × 0.3 × 0.5 mm.

Also, the present invention relates to the method in which the RRF protein crystal has respective unit lattices of a size of a=b=47.3Å and c=297.6Å.

Further, the present invention relates to the method in which the RRF protein crystal is characterized by a structure coordinate described in Table 7.

Also, the present invention relates to the method in which the RRF protein crystal is derived from Thermotoga Maritima.

Also, the present invention relates to the method in which the RRF protein crystal is orthorhombic.

Also, the present invention relates to the method in which

the RRF protein crystal has a space group P2<sub>1</sub>2<sub>1</sub>2.

Also, the present invention relates to the method in which the RRF protein crystal has a size of 30 × 50 × 250 µm.

Also, the present invention relates to the method in which the RRF protein crystal is derived from strain X.

Further, the present invention relates to the method in which the RRF protein crystal is crystallized by a drop-like vapour diffusion method.

Also, the present invention relates to the method in which the RRF protein crystal is a heavy atom derivative and the crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

Also, the present invention relates to the method in which the heavy atom derivative is formed by reaction of a compound selected from the group consisting of thyromethal, gold thiomalate, uranyl acetate and lead chloride.

Further, the present invention relates to the method in which the RRF protein crystal is a heavy atom derivative of platinum or mercury.

Also, the present invention relates to the method in which the RRF protein is a monomer.

Also, the present invention relates to the method in which the RRF protein is characterized by amino acid displacement according to Table 5 or Table 6.

Further, the present invention relates to the method in which a compound characterized by the chemical entity bound to the active site, accessory binding site or pocket is an inhibitor to the RRF protein.

Also, the present invention relates to the method in which the inhibitor is a competitive inhibitor, an uncompetitive inhibitor or a noncompetitive inhibitor to the RRF.

Also, the present invention relates to the method comprising determining orientation of a ligand at the active site or accessory binding site of the RRF protein.

Further, the present invention relates to the method in which the structure coordinate is a structure coordinate of the RRF protein according to Table 7.

Also, the present invention relates to the method in which the pocket of the RRF protein is a pocket in the vicinity of C-terminal positioned on a folded part separating two domains of the RRF protein.

Further, the present invention relates to the above-mentioned method in which the above-mentioned compound inhibits binding of the RRF protein to ribosome or inhibits the behavior of the RRF protein on ribosome.

The present invention also relates to an inhibitor of the RRF protein obtained by the above-mentioned method.

Also, the present invention relates to a method for searching a compound that can inhibit the activity of the RRF protein based

on the activity of inhibiting the binding of the RRF protein to ribosome or the activity of inhibiting the behavior of the RRF protein on ribosome.

Further, the present invention relates to an inhibitor of the RRF protein obtained by the above-mentioned method.

Also, the present invention relates to a method for determining the three-dimensional structure of RRF protein, including the steps of clarifying the crystal form of mutants, homologues or co-complexes of the RRF protein by molecular replacement.

The present invention also relates to an RRF protein crystal which is orthorhombic.

Also, the present invention relates to the RRF protein crystal having a space group  $P2_12_12$  and size of  $30 \times 50 \times 250 \mu\text{m}$ .

Also, the present invention relates to the RRF protein crystal in which the RRF is derived from strain X.

Also, the present invention relates to the RRF protein crystal which is bipyramidal.

Further, the present invention relates to the RRF protein crystal in which the RRF protein crystal has a space group  $P4_12_12_1$  or a space group  $P4_32_12$ .

Also, the present invention relates to the RRF protein crystal having a size of  $0.3 \times 0.3 \times 0.5 \text{ mm}$ .

Also, the present invention relates to the RRF protein crystal having respective unit lattices of a size of  $a=b=47.3\text{\AA}$  and  $c=297.6\text{\AA}$ .

Also, the present invention relates to the RRF protein crystal characterized by amino acid displacement according to Table 5 or Table 6.

Further, the present invention relates to the RRF protein crystal characterized by a structure coordinate according to Table 7.

Also, the present invention relates to the RRF protein crystal derived from Thermotoga Maritima.

Also, the present invention relates to the RRF protein crystal crystallized by a drop-like vapour diffusion method.

Further, the present invention relates to the RRF protein crystal in which the crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

Also, the present invention relates to an RRF protein in which amino acid in an active site is selected from the group consisting of Arg 110, Arg 129 and Arg 132 of SEQ. ID. NO. 1.

Also, the present invention relates to the RRF protein in which at least one amino acid in the active site or accessory active site is replaced by at least one amino acid selected from the group consisting of naturally occurring amino acids, non-natural amino acids, selenocysteine and selenomethionine.

Further, the present invention relates to the RRF protein in which a hydrophilic amino acid or a hydrophobic amino acid in the

active site or accessory active site is replaced.

Also, the present invention relates to the RRF protein in which at least one cysteine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine and selenomethionine.

Also, the present invention relates to the RRF protein in which at least one methionine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine or selenomethionine.

Further, the present invention relates to the RRF protein in which the RRF protein is in a crystal form.

Also, the present invention relates to the RRF protein having a specific activity higher or lower than that of a wild type enzyme.

Also, the present invention relates to the RRF protein having a varied substrate specificity.

Further, the present invention relates to use of the RRF protein for measuring binding interaction between a compound and the RRF protein.

Further, the present invention relates to the RRF protein in which at least one amino acid residue on a surface of the RRF protein, in the surface or in the vicinity thereof is replaced and a change in surface charge by one or more charge units occurs.

Now that presently it is presumed that RRF is an ideal target of antibacterial agents, the three-dimensional structure of RRF clarified by the present invention is extremely important in the

industry since it directly associated with the development of antibacterial agents and the like. In addition, in consideration of the fact that the primary structures of RRFs of many pathogens are very close to each other (for example, the RRF of Pseudomonas aeruginosa has 60% homology to that of Escherichia coli), also concerning the three-dimensional structure of RRF of other pathogens, its clarification becomes extremely easy by the data of the three-dimensional structure of the RRF according to the present invention. Therefore, also in order to develop species-specific antibacterial agents, the present invention is extremely useful in the development of next generation antibiotics, fungicides and dezymotizing agents on the basis of RRF inhibition, in particular as an index upon developing antibacterial agents by rational drug design.

The terms used in the present specification are defined as follows.

"RRF protein" means an RRF protein having an enzyme activity in an ordinary state.

"Naturally occurring amino acid" means an L-isomer of a naturally occurring amino acid. The naturally occurring amino acids are glycine, alanine, valine, leucine, isoleucine, serine, methionine, threonine, phenylalanine, tyrosine, tryptophane, cysteine, proline, histidine, aspartic acid, asparagine, glutamic acid, glutamine,  $\gamma$ -carboxyglutamic acid, arginine, ornithine and

lysine. Unless specifically indicated, amino acids in the present specification are L-forms.

"Non-natural amino acid" means an amino acid that is not naturally found in proteins. As examples of the non-natural amino acid used in the present specification, there can be cited racemi mixtures of selenocysteine and selenomethionine. Further, the non-natural amino acid includes D- or L-forms of norleucine, para-nitrophenylalanine, homophenylalanine, para-fluorophenylalanine, 3-amino-2-benzylpropionic acid, and homoarginine, and D-phenylalanine.

"Positively charged amino acid" includes any optional naturally occurring amino acid or non-natural amino acids having a positively charged side chain under normal physiological conditions. As examples of the positively charged naturally occurring amino acid, there can be cited arginine, lysine and histidine.

"Negatively charged amino acid" includes any optional naturally occurring amino acid or non-natural amino acids having a negatively charged side chain under normal physiological conditions. As examples of the negatively charged naturally occurring amino acid, there can be cited aspartic acid and glutamic acid.

"Hydrophobic amino acid" means any optional amino acid that has a relatively water-insoluble, uncharged and nonpolar side chain.

Examples of the naturally occurring hydrophobic amino acid are alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophane and methionine.

"Hydrophilic amino acid" means any optional amino acid that has a relatively water-soluble, uncharged and polar side chain. Examples of the naturally occurring hydrophilic amino acid are serine, threonine, tyrosine, asparagine, glutamine, and cysteine.

"Mutant" refers to an RRF polypeptide characterized by substitution of at least one amino acid in the RRF sequence of wild type E. coli (that is, polypeptide showing the biological activity of wild type RRF). Such a mutant can be obtained by the expression of cDNA of RRF in which mutation has occurred in the sequence encoded thereby, for example, by oligonucleotide specific induction. The RRF mutant can be obtained by a general biosynthetic method by Noren, C.J. et al. (Science, 224, p182-188 (1989)) by site specific incorporation of non-natural amino acids to the RRF protein.

Selenocysteine or selenomethionine is incorporated by wild type or mutant type RRF by the expression of cDNA encoding the RRF in auxotrophic E. coli strain. In this method, the wild type or mutant type RRF cDNA does not contain one (or both) of natural cysteine and natural methionine and can be expressed in a host on a growth medium enriched with selenocysteine or selenomethionine (or both). Further, selenomethionine can be incorporated into a wild type or mutant type RRF by a methionine metabolism inhibiting method (Van

Dyne, G.D. et al., J. M. B., 229 pp105 (1993)).

"Change in surface charge" means a change in at least one charge unit of a mutant polypeptide at a physiological pH in comparison with the wild type RRF. This can be obtained by mutation of at least one amino acid of the wild type RRF into an amino acid having a side chain having a charge different from that of the wild type side chain at a physiological pH. The change in surface charge can be determined by measuring the isoelectric point of the polypeptide having a substituted amino acid and comparing it with the isoelectric point of the wild type RRF molecule.

"Change in substrate specificity" refers to a change in substrate of the mutant RRF in comparison with the wild type RRF. The substrate specificity (species specificity) is determined by separating ribosome, tRNA and EF-G from a pathogen and based on whether or not they can be used as substrates for RRF of E. coli and RRF mutants.

"Kinetic form" refers to the state of an enzyme in a free form or in a non-bound form, or the state of an enzyme bound to a chemical entity either at its active site or an accessory active site.

"Competitive" inhibitor is an inhibitor that inhibits the RRF activity by binding to the same kinetic form of RRF as that to which the substrate of RRF binds, and therefore, by directly competing with the active site of RRF.

"Uncompetitive" inhibitor is an inhibitor that inhibits RRF

by binding to a different kinetic form of RRF from that to which the substrate binds.

"Noncompetitive" inhibitor is an inhibitor that binds to either the free form or substrate-bound form of RRF.

"Homologue" means a protein that has at least 30% amino acid sequence homology with RRF or any optional function domain of RRF.

"Co-complex" means RRF, mutant or homologue of RRF bound to a chemical entity or compound through a covalent bond or non-covalent bond.

" $\beta$ -Sheet" refers to a conformation of polypeptide chain extending in an expanded zigzag conformation. Polypeptide chain portions extending in parallel all extend in the same direction. The polypeptide chains extending in anti-parallel extend in the direction opposite to the direction of the parallel lines.

"Active site" or "active site portion" refers to any optional site or all sites in RRF as below. The substrate-binding site is a site to which ribosome and its complex binds and at which decomposition of the substrate occurs. The active site is in the vicinity of at least amino acid residue 110, 129, and 132 by use of SEQ. ID. No. 1.

"Structure coordinate" refers to a mathematical coordinate obtained according to a formula relating to the pattern obtained by the diffraction of X-ray monochromatic beam by an atom (dispersion center) of RRF molecule in the form of crystal. The dispersion data

is used for calculating an electron density map of the repeating unit of crystal and the electron density map is used for establishing the positions of respective atoms in the unit lattice of crystal.

"Heavy atom derivative" refers to a chemically modified form of RRF protein crystal. In making it, in actuality, the crystal is dipped in a solution containing a heavy metal atom salt or an organometal compound that can diffuse through the crystal and bind to the surface of a protein (for example, lead chloride, gold thiomaleate, thyromethal or uranyl acetate). The position or positions of bound heavy metal atom or atoms can be determined by X-ray diffraction analysis of the dipped crystal. Then, using the data, phase data used for constructing the three-dimensional structure of an enzyme are prepared. One skilled in the art will understand that the set of structure coordinate determined by X-ray crystallography has a standard error. For the purpose of the present invention, any set of structure coordinates of RRF, RRF homologue or RRF mutant having a root-mean-square value deviation of protein backbone atoms (N, Ca, C and O) of less than 0.75 Å when superposed on the structure coordinates enumerated in Table 7 should be considered the same.

"Unit lattice" refers to a block of a fundamental parallelohexahedron. Total volume of the crystal can be constructed by repeated regular stacking of such blocks.

"Space group" refers to an arrangement of objective elements

of a crystal.

"Molecular substitution" refers to a method including a step of orienting and positioning another molecule whose structure coordinates (for example, the structure coordinates shown in Table 7) are known in the unit lattice of an unknown crystal to thereby prepare a provisional model of RRF crystal whose structure coordinates are unknown such that the observed diffractive pattern of the unknown crystal can be optimally explained. Then, a phase is calculated based on this model and synthesized with the observed amplitude to obtain an approximate Fourier synthesis of the structure whose coordinates are unknown. Then, application to a purified substance enables one to finally obtain an accurate structure of the unknown crystal. By use of the structure coordinates of RRF of the present invention and by use of molecular substitution, the structure coordinates of a mutant, homologue, or co-complex or different crystal structure of RRF can be determined.

In examples of the present invention, crystallization and structural analyses were performed using strain X derived RRF and Thermotoga Maritima derived RRF. However, practice can also be made similarly on other RRFs. Also, upon crystallization, not only RRF protein itself but also, RRF protein mutants, RRF protein homologues, and RRF protein co-complexes can be crystallized and the respective structures can be analyzed.

"Pocket" refers to a hollow that is present on an RRF protein

surface and also includes in addition to a binding pocket that is present on a binding site or accessory binding site of an RRF protein, other pockets that do not participate in binding to a substrate and so forth upon the expression of the activity of RRF.

The present invention provides for the first time the crystals of RRF of strain X and of Thermotoga Maritima RRF and the structures of RRF determined therefrom. On the other hand, the crystal of Thermotoga Maritima RRF was formed from an ammonium sulfate solution. The crystal has space group P4<sub>3</sub>2<sub>1</sub>2 of a bipyramid type. The unit lattice of the crystal has  $a=b=47.3\text{\AA}$ ,  $c=297.6\text{\AA}$ . The structure coordinate of RRF is shown in Table 7. The crystal packing indicates that RRF is a monomer.

Fig. 3 shows an illustration of Thermotoga Maritima RRF by a ribbon. Helices A, B, C, D, E, and F indicate helices that exist from N-terminal toward C-terminal.  $\beta$ -Sheets 1, 2, 3, 4, 5, and 6 are numbers of  $\beta$ -sheets that exist from N-terminal toward C-terminal. As shown in the figure, RRF consists of 2 domains, one consisting of 3 helices and the 2nd domain being a complex of  $\beta$ -sheet coil and a helix. The active site mounts on the E and F helices in the figure and in order to maintain the activity, it is important to retain the three-dimensional structure of the domain including the helices B, C, and D and  $\beta$ -sheets 1, 2, 3, 4, and 5.

Fig. 4 represents a space-packing model of Thermotoga Maritima RRF and N and C indicate N-terminal and c-terminal, respectively.

The gray color represents a carbon atom, red represents an oxygen atom, violet represents an N atom. The number shows the SEQ. ID. Number of amino acid sequence and 1 designates N-terminal.

Thus, based on the data concerning the three-dimensional structure of RRF elucidated by the present inventors, the identification of the active site and accessory binding site of an enzyme has been made possible for the first time. It has revealed together with the results of RRF gene mutation described later that there is a high possibility that the active site portion contains at least amino acid residues Arg 110, Arg 129 and Arg 132 of SEQ. ID. NO. 1.

The present invention for the first time makes it possible to use a molecular design technology in which chemical entity and compound are designed, selected and synthesized with respect to RRF. The chemical entity and compound include inhibitory compounds that can bind to all or a portion of the active site or accessory-binding site of RRF. Upon approaches made possible by the present invention, a compound binding to an enzyme is designed and the structure coordinate of RRF is used in order to modify the physical properties (for example, solubility) of the compound in various methods. For example, the present invention makes it possible to design a compound that acts as a competitive inhibitor of RRF by binding all or a portion of the active sites of RRF. The present invention also makes it possible to design a compound that

acts as an uncompetitive inhibitor of RRF. These inhibitors can bind to all or a portion of the accessory binding sites of the RRF that has already bound to the substrate and can be more potent than the competitive inhibitor that binds only to the active site of RRF and more nonspecific. Similarly, noncompetitive inhibitors that inhibit RRF by binding thereto can be designed by use of structure coordinate obtained by the present invention regardless of whether it is bound or not bound to another chemical entity.

A second design approach is to confirm an RRF crystal based on molecules composed of various chemical bodies in order to determine an optimal site for the interaction between an RRF inhibitor candidate and RRF. For example, high resolution X-ray diffraction data recovered from a crystal that is saturated with a solvent makes it possible to determine the position of solvent molecules of each type. Then, a small molecule that strongly binds to these sites can be designed and synthesized and tests on its inhibitory activity can be performed (Travis, J., Science, 262, p1374 (1993)).

The present invention is useful in designing improved analogue of an RRF inhibitor or designing a novel class of inhibitors based on reaction intermediate of RRF and RRF inhibitor co-complex in the reaction of other compound that binds to substrate or RRF with the RRF. This provides a novel means for designing an RRF inhibitor having both high specificity and high stability.

Another approach that is made possible and facilitated by the

present invention is to perform screening by use of a computer on a chemical entity or compound that can bind to RRF entirely or partially. In this screening, the property of conformity of such a chemical entity or compound to the binding site can be judged by either shape complementarity or estimated interaction energy (Meng, E.C. et al. J. Comp. Chem., 13, 505-524 (1992)).

In the case where RRF can be crystallized in more than one crystal form, structure coordinate or a part of it of RRF as provided by the present invention is particularly important for the analysis of the structure of other crystal form of RRF. The structure coordinate or a part of it of RRF can also be used for the analysis of the structure of an RRF mutant, the structure of an RRF co-complex, or the structure of the crystal form of any other optional protein having a significantly homologous amino acid sequence to any optional functional domain of RRF.

One of the methods that can be used for this purpose is molecular substitution. In this method, whether or not an unknown crystal structure is the crystal form of another form of RRF, RRF mutant or RRF co-complex or any other optional protein having an amino acid sequence that is significantly homologous to any optional functional domain of RRF can be determined by use of the structure coordinate of RRF of the present invention as provided in Table 7. This method provides accurate structural form about an unknown crystal more quickly and efficiently than trying to determine such

data from the beginning.

Furthermore, according to the present invention, RRF mutants can be crystallized by way of its co-complexes with known RRF inhibitors. Then, a series of crystal structures of such complexes can be analyzed by molecular substitution and compared with the crystal structure of wild type RRF. Therefore, a promising site for modification among various binding sites of the enzyme can be identified. Based on the data, a means for determining the most effective binding interaction (for example, an increased hydrophobic interaction) between RRF and the chemical entity or compound is provided.

All the above-mentioned complexes can be studied by use of a known X-ray diffraction technology and made precise so as to have an R value of about 0.20 or less in comparison with 2 to 3 Å resolution

*Sub B1* X-ray data by use of a computer software (for example, X-POLAR, Yale University, 1992, distributed by Molecular Simulation, Inc) (for example, Blundell & Johnson, Protein Crystallography, Academic Press (1967), Methods in Enzymology, Vol. 114, 115, H.W. Wycoff et al., Academic Press (1985)). Therefore, the data can be used for optimizing an RRF inhibitor and more importantly, can be used for designing a novel RRF inhibitor and synthesize it. The structure coordinate of RRF provided in the present invention facilitates the identification of related protein, enzyme or nucleic acids similar to RRF in function, structure or both of them. This enables more

Sub B1  
cont

proper presumption of active site, binding site and so forth of RRF itself and the above-mentioned similar protein and the like, which leads to a novel antibacterial agents, herbicide or fungicide.

In designing a compound that binds to or inhibits the RRF of the present invention, generally two elements must be considered. First, the compound must physically and structurally bind to the RRF. As the non-covalent bond intermolecular interaction important for the binding of RRF to its substrate, there can be cited hydrogen bond, van der Waals force and hydrophobic interaction.

Secondly, the compound must be one on which a conformation that enables binding to the RRF can be supposed. A specified part of a compound may not directly participate in binding to the RRF but the part can still influence the whole conformation of the molecule. This also gives a considerable influence on the effectiveness. As the necessary conditions of such a conformation, there can be cited three-dimensional structure and orientation as a whole of a chemical entity or compound relating to all or a part of binding sites (for example, active site or accessory binding site of RRF), or distance between functional groups of a compound containing some chemical bodies that directly interact with the RRF.

Potential inhibitory effect or binding effect of a chemical compound on the RRF can be analyzed before the compound is actually synthesized and tested by use of a computer modeling technology. In the case where a theoretical structure of a predetermined compound

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suggests the existence of insufficient interaction and binding between the compound and the RRF, the synthesis and test of the compound can be avoided. However, in the case where the computer modeling suggests strong interaction, the molecule can be synthesized and its inhibitory capability can be tested by the method of Hirashima and Kaji (*Biochemistry*, 11, 4037 (1972)) or a method using an oligonucleotide, and in vivo screening (Japanese Patent Application No. Hei 10-158643). By this method, the synthesis of compounds that are ineffective can be avoided.

The inhibitory compounds of the RRF or other bound compounds of the RRF can be evaluated by a computer and chemical bodies or fragments can be designed by a means of a series of steps of screening and selecting their ability of binding to respective binding pockets or other regions of the RRF.

There may be used one of methods of screening the chemical bodies or fragments on their ability of binding to respective binding pockets of RRF, more particularly the binding site or accessory binding site of the RRF, or to other pockets not participating in binding to the substrate or the like upon expression of the activity of the RRF. This process can be started by visual study of the active site, for example, upon computer screening based on the RRF coordinate in Table 7. For example, as shown in the sketch by a ribbon in Fig. 3, the RRF that has a form of "L"-shape has a pocket in the vicinity of C-terminal positioned at the "L"-shaped bent portion that

separates the two domains. A compound bound to the pocket can be a leading candidate of an inhibitory compound to the RRF. The above-mentioned pocket can be readily observed by preparing a space-packing model based on the RRF coordinate shown in Table 7 by use of a software of Rasmol et al. The pocket is positioned between the two domains of the RRF and hence, it suggested the possibility that it participates in the activity of the RRF through adjustment of the angle between the domains. Then, the selected fragment or chemical entity can be positioned in various orientations or can couple to the respective binding pockets of the RRF. The coupling can be achieved by use of software such as Quanta and Sybyl and thereafter, minimization of energy and molecular kinetics are performed by use of a standard molecular mechanism force field (for example, CHARMM, AMBER).

A specialized computer program can aid the process of selecting a fragment or chemical entity. Examples of the programs include the followings:

*Sub B2*

The following program is available from Oxford University, oxford, UK: GPID (Goodford, P. J., "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules", *J. Med. Chem.*, 28, pp. 849-857 (1985)), and the following is available from Molecular Simulations, Burlington, MA: MCSS (Miranker, A or M. Karplus "Functionality Map of Binding Sites: A Multiple Copy Simultaneous Search Method.",

*Sub P2*  
cont

Proteins: Structure, Function and Genetics, 11, pp. 29-34 (1991)).

As for AUTODOCK (Goodsell, D. S. and A. J. Olsen, "Automated Docking of Substrates to Proteins by Simulated Annealing", Proteins: Structure Function and Genetics, 8 pp. 195-202, it is available from Scripps Research Institute La Jolla, CA, and as for DOCK (Kuntz, I., D. et al, "A Geometric Approach to Macromolecule-Ligand Interactions", J. Mol. Biol., 161, pp 269-288 (1982)), it is available from University of California, San Francisco, CA.

Once a proper chemical entity or fragment is selected, the chemical entity or fragment can be assembled into a single compound or inhibitor. The assembling can be performed by way of visual study of interrelationship fragments in a three-dimensional image displayed on a computer screen with respect to the structure coordinate of the RRF. Then, model construction is performed by a manual by use of software such as Quanta or Sybyl.

As examples of useful programs that can help one skilled in the art in the case where respective chemical bodies or fragments are contacted, there can be cited the followings:

The following program is available from the University of California, Berkeley, CA: CAVEAT (Bartlett, P. A. et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules", Molecular Recognition in Chemical and Biological Problems", Royal Chem, Soc., 78, pp. 182-196 (1989)). A region of 3D Database systems such as MACCS-3D (MDL Information Systems, San

Diego, CA is generally explained in Martin, Y. C., "3D database Searching in Drug Design", *J. Med. Chem.*, 35, pp. 2145-2154 (1992). As for HOOK, it is available from Molecular Simulations, Burlington, MA.

Instead of constructing an RRF inhibitor from one fragment or chemical entity at a time in a stepwise manner as described above, the inhibitory compound or other RRF bound compound can be designed wholly or anew by use of the active site (or one containing some parts of a known inhibitor as needed) from the RRF. As these methods there can be cited the followings:

The following program is available from Biosym Technologies, San Diego, CA: LUDI (Bohm, H. J., "The Computer Program LUDI: A New Method for the de novo Design of Enzyme Inhibitors", *J. Comp. Aid, Molec, Design*, 6 pp. 61-78(1992). As for LEGEND (Nishibata, Y. and A. Itai, *tetrahedron*, 47, p.8985 (1991), it is available from Molecular Simulations Burlington, MA. As for LeapFrog, it is available from Tripos Associates, St. Louis, MO.

Other molecular modeling can be used in the present invention. For example, the following should be referred: Molecular Modeling Software and Methods for Medicinal Chemistry, *J. Med. Chem.*, 33, p883-894 (1990) by Cohen, N. C., et al. or Navia, M. A. and M. A. Murcko, The Use of Structural Information in Drug Design, *Current Opinions in Structural Biology*, 2, p. 202-210(1992).

Once a compound is designed or selected by the above-mentioned

method, the effectiveness in that the compound can bind to the RRF can be tested by computer evaluation and then optimized. For example, for a compound that is designed or selected so as to function as an RRF inhibitor, preferably a volume must be studied that does not overlap the volume occupied by the active site in the case where it binds to a natural substrate. An effective RRF inhibitor must preferably show a relatively small difference in the energy between its bound state and free state (that is, in a small binding stress). Therefore, the most effective RRF inhibitor must be designed with a binding stress of not exceeding about 10 kcal/mol, preferably about 7 kcal/mol. The RRF inhibitor can interact with an enzyme in a similar conformation having an overall binding energy of more than 1. In such cases, the stress of binding is in a difference between the energy of the free compound and the average energy of conformations observed in the case where the inhibitor binds to the enzyme.

The compound designed or selected such that it binds to the RRF can be optimized by use of a computer in such a manner that preferably it does not have a repulsive electrostatic interaction with the target enzyme. As such a noncomplementary (for example, static charge) interaction, there can be cited repulsive charge-charge interaction, dipole-dipole interaction and charge-dipole interaction. Specifically, totaling all the electrostatic interaction between the inhibitor when it is bound

to the RRF and the enzyme, neutral or preferable contribution is made to the enthalpy of bond.

Specified computer software for evaluating the stress and electrostatic interaction of a compound can be utilized in this field of art. As examples of program designed for such uses, there can be cited Gaussian 92 C, M. J. Frisch, Gaussian, Inc., Pittsburgh, PA 1992; AMBER, version 4.0 P. A. Kollman, University of California, San Francisco, 1994; QUANTA/CHARMM Molecular Simulations, Inc., San Diego, CA 1994 and so forth. These programs can be practiced by use of a general computer such as Silicon Graphics IRIS 4d/35 or IBM RISC/6000 Model 1550 or the like. Other hardware and software are known to one skilled in the art.

Once an RRF bound compound is optimally selected or designed as described above, then substitution of some of atoms or side chains of the compound is performed in order to improve or modify the binding properties thereof. Generally, first substitution is conservative. That is, the substituent has substantially the same size, shape, hydrophobicity and charge as the original group. Those compounds of which it is known to change conformation in the art must be avoided. The chemical compounds thus substituted are analyzed of their effectiveness for conformity with the RRF in the same manner as the method by use of a computer as described above.

The present invention also makes it possible to make mutants of the RRF and elucidate their crystal structure. More specifically,

the present invention makes it possible to determine a desired site for mutation by the active site, accessory binding site and position of interface of the RRF on the basis of the crystal structure of the RRF.

For example, mutation may be directed to a specified site or combination out of sites of wild type RRF, that is, active site or accessory binding site only. Alternatively, for the induction of mutation, the position on the interface site is selected. Similarly, only the position on or near the enzyme surface may be substituted to generate a change in surface charge by 1 or more charge unit in comparison with the wild type enzyme. Alternatively, the amino acid residue of the RRF may be selected on the basis of its hydrophilic or hydrophobic property.

Such mutants are characterized by any of the different properties as compared with the wild type RRF. For example, such mutants may have a change in surface charge by 1 or more charge units or an increased stability to dissociation of subunits. Alternatively, such mutants may have a change in substrate specificity as compared with the wild type RRF or specific activity higher or lower than that of the wild type RRF.

The RRF mutant that is prepared by the present invention can be prepared by many methods. For example, the wild type RRF sequence can be mutated at a site that has been identified to be desirable for mutation by utilizing the present invention by use of an

oligonucleotide-specific mutation induction or other conventional technical (for example, depletion or the like) means. Alternatively, mutants of RRF can be made by site-specific substitution of a specified amino acid by an amino acid that does not naturally occur. Furthermore, the RRF mutants can be made by substitution of a specified cysteine or methionine residue by selenocysteine or selenomethionine. This is achieved by growing a host organism that can express either a wild type polypeptide or a mutant polypeptide on a growth medium that does not contain natural methionine or cysteine (or both) but is enriched with selenocysteine or selenomethionine (or both).

Mutation can be introduced in a DNA sequence encoding the RRF by use of synthetic oligonucleotides. The oligonucleotides include nucleotide sequence adjacent to a desired mutation site. Mutation can be made in a sequence of the full-length DNA sequence of RRF, RRF of other organism or shortened or elongated (deleted or added) RRF sequences.

According to the present invention, mutant RRF DNA sequences made by the above-mentioned method or substitute methods known in the art can be expressed by use of an expression vector. As is well known in the art, the expression vector contains an element that is typically independent of the host genome and enables self replication in the host cell and one or more phenotype markers for the purpose of selection. The expression vector also contains before or after an insert of a DNA sequence surrounding a desired RRF mutant

code sequence, a promoter, an operator, a ribosome-binding site, and a translation-starting signal and optionally a control sequence encoding a repressor gene and a stop signal. In some embodiments, in the case where secretion of produced mutant is desired, the nucleotide encoding the signal sequence may be inserted before the RRF mutant encoding sequence. For the expression under control of the control sequence, a desired DNA sequence must be operatively coupled to the control sequence. That is, it must have a suitable start signal before a DNA sequence maintaining a suitable leading frame that encodes the RRF mutant and enables the expression of this sequence under control by the control sequence and production of a desired product encoded by the RRF sequence.

A wide variety of well-known expression vectors that can be utilized are useful for expressing the mutated RRF encoding sequence of the present invention. These include vectors composed of segments of chromosomal DNA sequences, non-chromosomal DNA sequences and synthetic DNA sequences, such as, for example, various known derivatives of SV40, known bacteria plasmids (for example, *E. coli* derived plasmids such as col E1, pCR1, pBR322, pMB9 and derivatives thereof), plasmids of a wider host spectrum (for example, RP4), phage DNA (for example, many derivatives of  $\lambda$  phage (for example, NM989) and other DNA phages (for example, M13 and filamentous single strand DNA phage)), yeast plasmids such as  $2\mu$  plasmid or its derivatives, and vectors obtained by combination of plasmid and

phage DNA (for example, plasmid modified in order to utilize phage DNA or other expression control sequences). In a preferred embodiment of the present invention, the present inventors utilize E. coli vector.

Furthermore, any of a wide variety of expression control sequences that controls the expression of a DNA sequence when operatively coupled to the DNA sequence is used in a vector in order to express the mutated DNA sequence of the present invention. As such a useful expression control sequence, there can be cited, for example, early promoter and later promoter of SV40 for animal cells, lac system, trp system, TAC system or TRC system, major operator region and promoter region (all for E. coli) of  $\lambda$  phage control region of fd coat protein, promoter of 3-phosphoglycerate kinase or other sugar decomposing enzyme, promoter of acid phosphatase (for example, Pho5), promoter of yeast  $\alpha$ -mating factor for yeast, and other sequences known to control gene expression of prokaryote cell, eucaryote cell or virus and combinations thereof. In a preferred embodiment of the present invention, the present inventors utilize E. coli expression.

A wide variety of species of hosts are also useful for the production of mutant RRF according to the present invention. As such a host, there can be cited, for example, bacteria such as E. coli, Bacillus and Streptomyces, fungi such as yeast, animal cells such as CHO cell and COS-1 cell, plant cells and transgenic host

cells. In a preferred embodiment of the present invention, the host cell is E. coli.

It should be understood that when all the expression vectors and expression systems express the mutant DNA sequence of the present invention and produce modified RRF or RRF mutants, they do not always function in the same manner. Not all the hosts use the same expression system to equally function well. However, one skilled in the art can make selection from these vectors, expression control sequences and hosts without performing experiments or departing from the scope of the present invention. For example, the matter that is important when selecting vectors is the ability of a vector to replicate in a predetermined host. The number of copy of vector, ability of controlling the number of copy, and expression of other proteins to be encoded by the vector such as an antibiotic marker must also be taken into consideration.

Upon selecting the expression control sequence, various factors must be taken into consideration. These are, for example, relative strength of the system, its controlling power, conformity of DNA sequence encoding the modified RRF of the present invention, in particular conformity with respect to potential secondary structure.

The host must be selected in consideration of conformity with the selected vector, the toxicity of the modified RRF to the host, the ability of secreting a mature product, the ability of properly

folding the protein, fermentation requirement, easiness of purification of the modified RRF from the host, and safety. Among these parameters, one skilled in the art can select various vector/expression control system/host combinations that can produce a useful amount of mutant RRF.

The mutant RRF produced in these systems can be purified various conventional steps and strategies including steps and strategies used for purifying the wild type RRF.

Once RRF mutation is made at a desired position (that is, active site or accessory binding site), the mutant can be tested on any one of some objective properties.

*Sub B3*

For example, the mutant may be screened on a change in charge at a physiological pH. This can be determined by the isoelectric point of the mutant RRF in comparison with the isoelectric point (pI) of the wild type parent. The isoelectric point can be measured by gel electrophoresis by the method of Wellner, D., *Analyt. Chem.*, 43, p597 (1971). The mutant in which surface charge has changed is an RRF polypeptide having a substituted amino acid positioned at a surface of the enzyme and a changed pI as provided by the structural data of the present invention.

Furthermore, the mutant may be screened with respect to specific activity that is high or low as compared with the wild type RRF. The mutant is measured of its activity by use of the method of Hirashima and Kaji and the assay by use of oligonucleotide (cited

above). The mutant can be tested on a change in RRF substrate specificity by measuring the RRF reaction as described above.

Furthermore, an object of the present invention includes a mutant having increased safety. The RRF mutant having increased safety includes one that exhibits no loss of enzyme activity.

Hereinafter, the present invention will be illustrated in detail by examples. The examples shown below are merely for the purpose of detailed explanation thereof but by no means are meant to exclude other methods.

[EXAMPLES]

Example 1. Crystallization of RRF protein of strain X by drop-like vapour diffusion technique

5 µl of a solution containing 4 mg/ml to 8 mg/ml of RRF protein of strain X, 50 mM Tris hydrochloride, pH 8.5, 70-100 mM of sulfuric acid salt and 14% to 18% of polyethylene glycol was converted into droplets and equilibrated in a liquid pool containing a crystallizing reagent having a higher concentration than that of the droplets. The equilibration was performed until the vapour pressure of droplets became identical to the vapor pressure of the liquid pool due to diffusion of the volatile medium (water or organic solvent). When the equilibration occurred due to water exchange (from the droplets to the liquid pool) the volume of the droplets was changed. As a result, the concentrations of all the media in the droplets changed.

In case of the medium having a higher vapour pressure than that of water, exchange from the liquid pool to the droplets occurred. In the instant example, the glass vessel that the RRF protein solution contacted was used after its surface was subjected to hydrophobic treatment. By dialysis against a buffer composed of 100 mM of Tris hydrochloride, pH 8.5, 150 mM to 200 mM of sulfuric acid salt, 28% to 36% of polyethylene glycol, XRRF crystal was obtained. The crystal grew to a size of 30 × 50 × 250 μm over 1 to 3 weeks. The results are shown in Fig. 1.

Example 2. Three-dimensional structure of RRF by X-ray diffractive analysis

As a means for determining the RRF three-dimensional structure, a multiple isomorphous replacement procedure was used. This is a standard method necessary for obtaining diffusion data of a heavy atom from isomorphous protein crystal. A difference between the unreplaced one and the isomorph was calculated from the positions of the heavy atom to form a Patterson map. In preparing a protein model, the data on initial protein phase necessary for the calculation of electron density diagram were calculated by use of several kinds of derivatives.

The X-ray diffraction data of the refrigerated crystal were collected in BL71 by MaxII synchrotron (Sweden, Lund).

The native crystal was diffracted at a resolution of 2.6 Å.

Because of the problem of mosaicity of 1.5 or more, a resolution of 2.9 $\text{\AA}$  or less was thus far used. This typical diffraction pattern is shown in Fig. 2.

The native data analysis was completed and R<sub>sym</sub> was found 1.0. The statistical data are shown in Fig. 1.

The crystal has  $a=98.5\text{\AA}$ ,  $b=106.7\text{\AA}$ , and  $c=66.7\text{\AA}$  and belongs to P2<sub>1</sub>2<sub>1</sub>2.

The asymmetric unit includes 2 to 4 molecules and there are translations of 0.5, 0.33 and 0.5 between the molecules. Data of two derivatives were obtained and the derivative of platinum diffracted at 4.0 $\text{\AA}$  and the derivative of mercury diffracted at 3.8 $\text{\AA}$ .

#### Statistical study of native data

Table showing summary of diffractive intensity and R-factor indicated in terms of the size of shell (resolution)

Value of R (as a linear function) = 3D SUM (ABS(I-<I>))/SUM  
(I)

Value of R (as a quadratic function) = 3D SUM ((I-<I>)\*\*2)  
/ SUM (I\*\*2)

$$\chi^2 = 3D \text{ SUM } ((I - \langle I \rangle)^2) / (\text{error}^{**2 * N} / (N - 1))$$

For all calculations of addition, calculation was performed only on values measured twice or more.

Table 1

Lower limit and upper limit of shell Angstrom	Diffraction intensity	Average	Normal	Linear multiplier	Quadratic multiplier		
Lower limit	Upper limit	Average	Error	Stat. value	$\chi^2$ value	R-factor	R-factor
30.0	7.12	814.6	36.6	18.5	0.709	0.033	0.032
7.12	5.67	227.1	16.7	13.5	1.012	0.084	0.072
5.67	4.95	266.0	19.0	15.3	0.983	0.083	0.075
4.95	4.50	417.3	25.3	18.4	1.052	0.070	0.064
4.50	4.18	394.0	25.5	19.6	1.239	0.087	0.086
4.18	3.93	330.4	24.4	19.7	1.064	0.093	0.088
3.93	3.74	296.1	24.6	20.9	1.286	0.125	0.219
3.74	3.58	283.8	25.5	22.0	1.275	0.142	0.221
3.58	3.44	207.5	23.2	21.2	1.314	0.170	0.192
3.44	3.32	173.2	22.5	21.1	1.278	0.193	0.298
3.32	3.22	151.8	22.1	20.9	1.414	0.222	0.231
3.22	3.12	130.4	21.7	20.8	1.560	0.265	0.280
3.12	3.01	108.3	20.6	19.9	1.552	0.306	0.307
3.04	2.97	92.2	19.9	19.2	1.655	0.334	0.315
2.97	2.90	74.9	19.2	18.7	1.632	0.411	0.416
Total		268.4	23.2	19.3	1.259	0.119	0.102
reflection							

Example 3. Crystal structure of RRF of Thermotoga Maritima

RRF cDNA of Thermotoga Maritima was cloned in an expression vector (PET1650) and expressed in E. coli by addition of IPTG. As a result, Thermotoga Maritima RRF accumulated in the host cells at a high level. The cells were mechanically destroyed and purified

by a method which is modified from the method of Hirashima and Kaji (*Biochemistry*, 11, 4037, (1972)) to obtain *Thermotoga Maritima* RRF. The crystal of RRF was grown by vapour diffusion. Mixing 5-10  $\mu$ l of the RRF solution with the same amount of reservoir liquid (0.1 M of sodium acetate, 2.0 M of ammonium sulfate (pH 5.5), 5 mM of DTT, and 10% of glycerol), equilibrating the mixture with 600  $\mu$ l of the above-mentioned reservoir liquid at 25°C, and streaking this liquid for 24 hours to accelerate crystal formation resulted in the appearance of crystal after 15 hours. Then, after 3 days, this grew into a crystal of bipyramidal type of  $0.3 \times 0.3 \times 0.5$  mm.

It is possible for one skilled in the art to properly modify the above-described crystallization conditions.

All the X-ray dataset (2.55 $\text{\AA}$  resolution) were collected in a Mar 345 Image Plate Detector by use of MAXII synchrotron in BEAMLINE BL711. Merge, scale, indexing and integration of data were performed by use of programs of VDS and Xscale (Kabsch, W. J. *Appl. Crystallography* 26 795 (1993)). MAD data (multiwavelength anomalous dispersion data) were performed in BEAMLINE BM14 ESRF at a wavelength of 0.9184 to 0.978 and 0.9788  $\text{\AA}$  and collected by use of a Mar 345 Image Plate Detector. The data were processed by use of Mosflm (Leslie, A. G. W. in *Crystallographic computing oxford Univ Press* (1990)), and scale and merge were performed in Scala (CCP4).

For the position of selenium atom in the RRF, shelx program

(sheldrick, G. M. Acta Cryst. A46 P467 (1998)) was used and a normalized structural factor was used. A heavy atom (selenium) parameter was made precise by use of MIphase (CCP4). Trial made to obtain electron density maps based on both space groups P4<sub>1</sub>2<sub>1</sub>2 and P4<sub>3</sub>2<sub>1</sub>2 revealed that correct space group was P4<sub>3</sub>2<sub>1</sub>2. An average merit value indicated a resolution of 0.66 Å to 4.0 Å. Table 2 shows the crystal data of Thermotoga Maritima RRF.

Table 2

Data collection

The highest resolution shell, 2.65 - 2.55 Å

Resolution	30-2.55
Total observations	79947 (7119)
Unique reflections	11927 (1261)
Average redundancy	6.7 (5.6)
R <sub>sym</sub> (%)	0.049 (0.156)
Data completeness (%)	99.8 (99.1)
I/sigma(I)	26.4 (8.9)

$R_{\text{merge}} = (\sum |I - \langle I \rangle| / \sum I)$  where I is the observed intensity and  $\langle I \rangle$  is the average intensity of symmetry-related reflections.

Values in parentheses refer to the values at maximum resolution.

The map was improved by solvent flattening and phase expansion (CCD4-collaborative conputity project #4, A suite of program for protein crystallography Daiesburg Laboratory, Warrington, WA4 4. AD UK (1979) and it was successful in tracing a complete polypeptide chain. Precision ((CNS) ranger A. T. et al., Acta Cryst D54 p905 (1998)) of the position of model construction program (Jones, A.T. et al., Acta Cryst. A47 PP110 (1991)) and phase combination were

repeated to thereby enable all the side chains to be introduced into the model. Rigid body and positional precision were performed and further simulated annealing was carried out. This model was compared with the crystal data (native data) to reach a final model only by use of the phase of the model.

The model of the RRF of the present invention has an R factor (25.3%) for all the observed data on X- and Y-axes. Root-mean-square value deviation from ideal bond length and bond angle are 0.01 $\text{\AA}$  and 2.0 $\text{\AA}$ , respectively.

Table 3 shows results of statistical processing of Thermotoga Maritima RRF crystal data.

Table 3

Data collection statistics

Dataset (wavelength $\text{\AA}$ )	Peak (0.9786)	Inflection (0.9788)	Remote (0.9184)
Resolution ( $\text{\AA}$ )	2.9	2.9	2.9
Completeness (%)	99	98	98
Rsym (%)	7.0	7.0	7.2
Cullis R-centric	0.67	0.56	-
Cullis R-anomalous	0.60	0.77	0.78

Table 4 shows phasing of Thermotoga Maritima RRF.

Table 4 shows Phasing of Thermotoga Maritima RRF

Table 4

Resolution

Phasing						
Resolution bin (Å)	30 - 11.5	11.5 - 8.1	8.1 - 6.2	6.2 - 5.1	5.1 - 4.3	4.3 - 3.7
FOM	0.704	0.732	0.745	0.683	0.623	0.58
Mean FOM	0.66					

2. Presumption of the active site of RRF

To presume the position of active site in the RRF molecule, a series of RRF mutants were produced. Mutation induction was performed by use of a PCR method that involved many errors to introduce mutation (Janosi et al., EMBO J. 17 1141 (1998)).

Isolation of a plasmid having frr (gene encoding RRF) having a lethal gene mutation was performed as follows. pMIX described in Janosi et al., EMBO J. 17 1141 (1998) was used. To explain briefly, pMIX is a plasmid obtained by causing various gene mutations to occur in frr and introducing the frr into a chloramphenicol-resistant plasmid. In this example, Escherichia coli LJ4 (recA-) was used as a host. Since this bacterium has on chromosome frr inactivated by frame shift, so that the Escherichia coli keeps life by means of wild type frr on pPEN(1560) (Janosi et al., EMBO J. 17 1141 (1998)). PPEN(1560) includes kanamycin resistant factor and sucrose sensitivity gene.

The Escherichia coli was transformed with pMIX and selected with chloramphenicol resistance as a marker. Since frr is indispensable to bacteria, the bacteria having a lethal mutation in pMIX cannot live without having the above-mentioned pPEN1560. Therefore, bacteria having both plasmids, pMIX and pPEN1560 were searched. Incidentally, the both plasmids, pMIX and pPEN1560 do not usually live together since they are incompatible. However, they live together if they are driven by necessity (necessity of antibiotic marker and frr) as described above.

To select such an Escherichia coli, the transformant was inoculated on a plate containing CM and sucrose, and further was replica plated on a plate containing CM and KM. Selecting a bacterium that grows in the latter but does not grow in the former enables selection of a bacterium that has pPEN1560 and lethal frr in pMIX. Since this bacterium has pPEN1560, it cannot grow on a plate containing sucrose. Out of 153 transformants thus obtained respective plasmids were purified with which Escherichia coli DH5 $\alpha$  (having wild type frr) was transformed. Since this bacterium has wild type frr as described above, it does not require pPEN1560 (kanamycin resistance). Therefore, selecting chloramphenicol- and kanamycin-sensitive Escherichia coli DH5 $\alpha$  enables selection of Escherichia coli having a lethal mutation and having pMIX.

From the thus obtained and Escherichia coli, plasmids were isolated and KpnI-HindIII fragment (0.9 kb, frr) was taken out and

DNA sequence determination by a common method was performed. The results are shown in Table 5.

Table 5 Genetic mutations inactivating RRF<sup>†</sup>

Mutational class	Allele	Nucleotide change	Change in the primary sequence of RRF	Notes	
<b>Single AA change</b>					
<i>frf146</i>	1	T(52)C	Leu(51)Pro	-	
<i>frf160</i>	1	T(161)C	Leu(54)Pro	-	
<i>frf161</i>	1	T(194)C	Leu(65)Pro	-	
<i>frf169</i>	1	T(99)C	Leu(65)Pro	Ser(32)silent	
<i>frf106</i>	1	T(194)C	Arg(110)His	Val(41)silent	
<i>frf119</i>	3	C(123)T	Arg(129)Cys	promoter involved	
<i>frf114</i>	1	C(-91)A	Arg(132)Gly	-	
<i>frf132</i>	1	C(394)G	Arg(132)Cys	-	
<i>frf133</i>	1	C(394)T	Arg(132)His	-	
<i>frf138</i>	1	G(395)A	Arg(132)Gln	-	
<i>frf124</i>	2	T(524)C	Leu(175)Pro	-	
<i>frf149</i>	2	C(447)T	Leu(175)Pro	Ser(149)silent	
<b>Double AA change</b>	<i>frf165</i>	1	G(28)A A(490)C	Glu(10)lys	-
<i>frf113</i>	1	G(28)C G(162)A A(490)C	Thr(164)Pro	Leu(154)silent	
<b>Class B</b>	<i>frf112</i>	1	T(38)C T(51)C	Glu(10)lys	-
<i>frf116</i>	2	T(107)A C(317)A	Met(13)Thr	-	
<i>frf118</i>	1	A(269)G G(329)A	Leu(36)Gln	-	
<i>frf134</i>	1	T(14)C A(103)G T(199)A	Asn(90)Ser	Thr(106)lys	
<b>Triple AA change</b>	<i>frf141</i>	1	G(88)A T(97)C C(994)T	Arg(110)His	Arg(132)Cys
<b>Class C</b>	<i>frf141</i>	1	G(88)A T(97)C C(994)T	Leu(65)Glu	-
<i>frf127</i>	1	G(52)T T(416)C	Arg(133)Pro	-	
<i>frf123</i>	1	A(76)T	Glu(18)stop	(17 AA, long RRF)	
<i>frf158</i>	1	C(135)G	Lys(26)stop	(25 AA, long RRF)	
<i>frf125</i>	1	C(157)T	Tyr(45)stop	(44 AA, long RRF)	
<i>frf162</i>	1	T(24)C	Gln(53)stop	(52 AA, long RRF)	
<i>frf140</i>	1	A(396)T T(204)C G(389)T	Gln(55)stop	(52 AA, long RRF)	
<i>frf110</i>	1	C(218)A	Lys(66)stop	(65 AA, long RRF)	
<i>frf131</i>	1	C(-6)A C(218)A	Ser(73)stop	(72 AA, long RRF)	
<i>frf108</i>	1	G(364)T A(540)G	Ser(73)stop	(72 AA, long RRF)	
<i>frf117</i>	1	A(430)T	Glu(122)stop	(121 AA, long RRF)	
C-terminal truncation via early stop			Lys(144)stop	(143 AA, long RRF)	
			+mutation beyond stop	-	
				+2 mutations beyond stop	
				SD-initiation spacer involved	

<i>fri136</i>	1	T(C336)C	A(430)T	Lys(44)stop	(143 AA long RRF)	Asp(112)silent
<i>fri159</i>	1	A(46)C	A(508)T	Lys(470)stop	(169 AA long RRF)	+mutation between promoter and SD
<i>fri142</i>	3	G(51)T		Glu(172)stop	(171 AA long RRF)	
C-terminal truncation & single AA change				Ser(35)Gly	Glu(53)stop (52 AA long RRF)	-
<i>fri15</i>	2	A(103)G	C(157)T	Asp(9)Gly	Glu(122)stop (121 AA long RRF)	-
<i>fri151</i>	1	A(11)G	G(66)T	Lys(21)Glu	Glu(123)stop (122 AA long RRF)	-
<i>fri140</i>	1	A(61)G	C(367)T	Lys(21)Glu	Gin(123)stop (122 AA long RRF)	-
<i>fri166</i>	1	A(61)G	G(162)A	C(367)T	Lys(21)Glu	Leu(154)silent
Class E		A(445)G	C(469)T	Set(149)Gly	Gln(157)stop (156 AA long RRF)	-
<i>fri121</i>	1	C(467)T	C(469)T	Ser(156)Phe	Gln(157)stop (156 AA long RRF)	-
<i>fri152</i>	1	C(467)T	C(469)T	Ser(156)T	Gln(157)stop (156 AA long RRF)	mutation beyond stop
<i>fri139</i>	1	C(467)T	C(469)T	C(555)T		
C-terminal truncation preceded by frame-shift				Stop at nt 50-52	(16 AA long RRF)	Ser(3) to Cys(16) changed
<i>fri170</i>	1	T(5)del		Stop at nt 50-52	(16 AA long RRF)	Asp(14) to Cys(16) changed
<i>fri101</i>	1	G(40)del		Stop at nt 50-52	(16 AA long RRF)	Ile(6) to Ser(56) changed
<i>fri169</i>	1	A(70)del		Stop at nt 170-172	(56 AA long RRF)	Ile(27) to Ser(56) changed
<i>fri143</i>	1	A(79)del		Stop at nt 170-172	(56 AA long RRF)	Ser(25) to Ser(56) changed
<i>fri129</i>	1	C(75)del		Stop at nt 170-172	(56 AA long RRF)	Ser(35) to Ser(66) changed
<i>fri126</i>	1	C(101)del	A(419)T	Stop at nt 170-172	(56 AA long RRF)	+mutation beyond stop
Class F		T(170)del	A(359)T	T(492)C	Stop at nt 176-178	Val(57) to Thr(58) changed
<i>fri105</i>	1				(58 AA long RRF)	+2 mutations beyond stop
<i>fri147</i>	1	C(G(82-83)del		Stop at nt 210-212	(69 AA long RRF)	Arg(28) to Val(69) changed
<i>fri153</i>	1	AT(199-200)C		Stop at nt 266-268	(88 AA long RRF)	Ile(67) to Giv(88) changed
<i>fri107</i>	1	A(333)del		Stop at nt 338-340	(112 AA long RRF)	Asp(112) changed
<i>fri103</i>	1	C(362)del		Stop at nt 416-418	(138 AA long RRF)	Ala(121) to Lys(138) changed
<i>fri137</i>	1	A(349)del	A(363)GA(501)G	Stop at nt 416-418	(138 AA long RRF)	Ile(116) to Lys(138) changed
						+mutation in shifted sequence
						+mutation beyond stop
<i>fri145</i>	1	A(389)del		Stop at nt 416-418	(138 AA long RRF)	Asn(130) to Lys(138) changed
<i>fri135</i>	1	A(511)del		Stop at nt 545-547	(181 AA long RRF)	Ile(168) to Glu(181) changed

<sup>†</sup>In description of nucleotide and amino acid changes, the positions of change are indicated by a number in parenthesis preceded by description of the wild-type nucleotide or amino acid and followed by mutated ones. The amino acids are described by their three letter codes. Abbreviations: AA=amino acid; del=deletion

As shown in this table, 61 strains were obtained. These had 53 different genotypes. It was confirmed that the thus separated plasmid having a lethal gene did not function as frr by use of LJ4 having temperature-sensitive RFF (Janosiet al., EMBO 17 1141 (1998)). All the obtained plasmids were not able to support the growth of LJ4 at 42°C.

Then, a method of separating amino acid mutation that does not influence the function of frr from the structural gene of frr will be described. For this purpose, LJ4 was used as a host. Since the frr on chromosome of this host does not function as described above, it can exist at 27°C by means of plasmid pKH6 having frr14.

Since this Escherichia coli lives by means of frr14 (that encodes temperature-sensitive RRF), naturally it is temperature-sensitive. When the Escherichia coli was grown at 27°C at a natural reversion rate, one that was grown at 42°C were obtained in a ratio of  $4.2 \times 10^{-6}$ . Of the Escherichia coli one that becomes temperature-sensitive again by replacing the plasmid with one having tsfrr(pKH6) was selected and the DNA sequence of the frr portion was determined by a common procedure. In all the frrs thus obtained, the gene mutation Val 117 Asp of frr returned to wild type valine. Several kinds of them showed mutation at amino acid sites other than the 117-position. The mutations showed no influence on the function of frr. The mutations are shown in Table 6.

**Table 6**  
*Genetic mutations reverting the temperature sensitivity of RRf<sup>a</sup>*

Allele	Phenotype	Number of isolates	Nucleotide in position..	Amino acid in position..						Notes
<i>rrf</i>	wf	NA	T	G	A	A	T	Val	Asp	Ile
<i>rrf14</i>	ts	NA	A	G	A	A	T	Asp	Asp	{22}
<i>rrf201</i>	tr revertant	2	T	G	A	A	T	Val	Asp	{2785}
<i>rrf206</i>	tr revertant	3	T	T	A	T	T	Val	Tyr	-
<i>rrf204</i>	tr revertant	1	T	T	A	T	A	Val	Tyr	Phe
<i>rrf202</i>	tr revertant	3	T	G	A	T	A	Val	Asp	Leu
<i>rrf203</i>	tr revertant	1	T	G	A	A	A	Val	Asp	Ile
<i>rrf205</i>	tr revertant	4	T	G	C	T	T	Val	Ala	Ile{171}silent
									Phe	-

<sup>a</sup>Amino acids are represented by their 3-letter codes. Abbreviations: NA=not applicable; wf=wild-type; ts=temperature sensitive;  
 tr=temperature resistant

### 3. Presumption of function mechanism of RRF

From the sketch by ribbon of RRF shown in Fig. 2, the space packing model shown in Fig. 3 and so forth, it revealed that the RRF has a shape and size similar to transfer RNA (Selmer, M., Al-Karadaghi, s., Hirokawa, G., Kaji, A. & Liljas, A., Science 286, 2349-2352 (1999)). Therefore, the possibility is suggested that the RRF expresses protein translation termination complex releasing activity by showing a behavior similar to that of transfer RNA. Specifically, a model as shown in Fig. 5 is suggested on the function mechanism of the RRF.

First, an RRF 4 binds to the aminoacyl site (A site) of a termination complex 6 (a) composed of transfer RNAs 2a, 2b, a messenger RNA 3 and a ribosome 1. To the RRF 4, an EFG 5 with GTP binds. Also, to the peptidyl site (P site) and exit site (E site) of the ribosome 1, the transfer RNAs 2a, 2b bind, respectively (b). Then, ribosome-dependent hydrolysis of GTP and translocation of RRF4 bound to the A site to the P site are caused by the EFG 5. At the same time, release of the transfer RNA 2b bound to the E site and release of the transfer RNA 2a bound to the P site via the movement to the E site take place and finally two molecules of transfer RNA are released (c). Finally, subsequent to the release of the RRF 4 and of the EFG 5 from the ribosome 1, the ribosome 1 is released from the messenger RNA 3 to complete the dissociation of the termination complex 6 (d).

To verify the hypothesis on the basis of this model, the following experiments were performed.

Example 4. Inhibition of the RRF activity by aminoglycosides

Aminoglycosides such as streptomycin, paromomycin, and gentamycin are known to inhibit themselves from binding to the A site of the transfer RNA by binding to the A site of ribosome (Moazed, D. & Noller, H. F., Nature 327, 389-394 (1987); Fourmy, D., Yosizawa, S. & Publisi, J. D., J. Mol. Biol., 277, 333-345 (1988)); Yoshizawa, S., Fourmy, D. & Publisi, J. D., EMBO J., 17, 6437-6448 (1988)). Therefore, according to the model in Fig. 5, the above-mentioned aminoglycosides should inhibit the binding of RRF to the A site and if such a binding is inhibited, the dissociation process of termination complex due to the RRF should also be inhibited. Accordingly, whether the dissociation process of termination complex is inhibited or not in the presence of the above-mentioned aminoglycosides was examined by use of the amount of transfer RNA released from the ribosome and the amount of ribosome released from the messenger RNA as indices.

The release of deacylating transfer RNA from ribosome was examined by the following method.

Polysome (Hirashima, A. & Kaji, A., J. Mol. Biol., 65, 43-58 (1972)) obtained from E. coli Q13 strain treated with tetracycline (0.6 to 1.8  $A_{260}$  unit) was incubated in 550  $\mu$ l of buffer R (10 mM Tris-Cl, pH 7.4, 8.2 mM magnesium sulfate, 80 mM ammonium chloride,

and 0.14 mM dithiothritol (DTT)) in the presence of 275  $\mu$ M of puromycin, 0.2 nmole of RRF, 0.2 nmole of EFG (Kaziro, Y., Inoue-Yokosawa, N. & Kawakita, M., *E. coli J. Biochem.* 72, 853-863 (1972)) and 0.37 mM of GTP at 30°C for 15 minutes. Then, as the aminoglycosides, streptomycin, paromomycin or gentamycin was added in an amount of 200  $\mu$ M, 100  $\mu$ M or 100  $\mu$ M, respectively. Then, by centrifugation at 330 G for 40 minutes by use of Microcon 100 (produced by Millipore, trade name), the released transfer RNA was separated from the termination complex. Then, to the above-mentioned Microcon 100, 550  $\mu$ l of buffer J (10 mM Tris-Cl, pH 7.6, 10 mM magnesium sulfate, 50 mM ammonium chloride, and 0.5 mM DTT) was poured and the mixture was centrifuged to wash the filter once. The combination of the washing solution and filtrate was centrifuged at 14,000 G for 15 minutes twice by use of Microcon 30 (produced by Millipore, trade name) to concentrate it to 14  $\mu$ l. Then, the concentrated transfer RNA was aminoacylated with 0.15  $\mu$ Ci of  $^{14}$ C-amino acid mixture (produced by Amersham, 52 mCi per 1 mg of carbon atom) dissolved in 30  $\mu$ l of a buffer solution (50 mM Tris-Cl, pH 7.8, 10 mM magnesium acetate, 6 mM  $\beta$ -mercaptoethanol, 3 mM ATP, 5 mM phosphoenolpyruvic acid, 138  $\mu$ g of pyruvate kinase, 33.3  $\mu$ g of aminoacyl transfer RNA synthetase (Monmose, K. & Kaji, A., *Arch. Biochem. Biophys.*, 111, 245-252 (1965))). The thus obtained radioactivity that is insoluble in cold trichloroacetic acid (4°C) corresponds to  $^{14}$ C-aminoacyl transfer RNA and the amount thereof was calculated on the basis of the

radioactivity of a known amount of transfer RNA labeled by the same method. The aminoglycosides used are produced by Sigma Co. Also, the termination complex was obtained from natural polysome of E. coli treated with puromycin (Hirashima, A. & Kaji, A., J. Biol. Chem., 248, 7580-7587 (1973)). It has been known that each ribosome in the isolated polysome in the stage of after completion of translocation and generally bear two molecules of transfer RNA (Remme, J., Margus, T., Villemans, R. & Nierhaus, K. H. Eur. J. Biochem. 183, 281-284 (1989)); Stark, H. et al., Cell 88, 19-28 (1977)).

The results are shown in Fig. 6. In Fig. 6, positive control is a value obtained when RRF, EFG and GTP were added without adding aminoglycosides while negative control is a value obtained when none of aminoglycosides, RRF, EFG and GTP was added.

The release of ribosome from messenger RNA was examined by the following method.

The above-mentioned polysome (0.5 to 0.8  $A_{260}$  unit) was incubated in 270  $\mu$ l of buffer R in the presence of 275  $\mu$ M of puromycin, 1 nmole of purified RRF (Hirashima, A. & Kaji, A., Biolchemistry, 11, 4037-4044 (1972)), 1 nmole of EFG<sup>32</sup>, 0.37 mM of GTP and aminoglycosides at 30°C for 15 minutes. As the aminoglycosides, streptomycin, paromomycin or gentamycin was added in an amount of 100  $\mu$ M, 5  $\mu$ M or 5  $\mu$ M, respectively. Then on 5 ml of sucrose with a density gradient of 15 to 30% in the buffer J, the above-mentioned incubated buffer solution was stacked and centrifuged under the

conditions of 40,000 rpm for 75 minutes at 4°C by use of Beckman SW50.1. The absorbance at 254 nm was monitored by an ISCO UA-6 detector and the concentration of free 70S ribosome was measured. The results are shown in Table 7. The values in Table 7 were expressed in percentage of the concentration of free 70S ribosome in the presence of aminoglycosides to the concentration of free 70S ribosome in the case where no glycoside was added (control). In control, about 42% of total ribosome (occupying approximately 90% of polysome) was converted into monosome by the RRF.

Table 7      Release of ribosome from mRNA by RRF and EF-G in the presence of various inhibitors

Inhibitor	Concentration	Release of ribosome from mRNA by RRF (percentage to control)
Control	-	100*
Paromomycin	5 $\mu$ m	16.5
Gentamycin	5 $\mu$ m	0
Streptomycin	100 $\mu$ m	9.9
Thiostreptone	20 $\mu$ m	0
Viomycin	50 $\mu$ m	0
Fusiginic acid	200 $\mu$ m	0
GMPPCP	370 $\mu$ m****	0

From Fig. 6, it can be seen that in the presence of the aminoglycosides, the release of transfer RNA was inhibited to a value identical to or less than that of the negative control. Also, from Table 7, it can be seen that in the presence of the aminoglycosides, the release of ribosome was also inhibited. These results strongly suggest that coupling of the RRF to the A site of ribosome is necessary for the expression of the activity of RRF. Therefore, it can be considered that the substance that inhibits binding of the A site of the RRF can be a potent candidate of an RRF inhibitor.

Example 5. Inhibition of RRF activity by thiostreptone and viomycin

Thiostreptone and viomycin are both EFG inhibitors and are known to inhibit the translocation of transfer RNA (Pestka, S., Biochem. Biophys. Res. Commun. 40, 667-674 (1970); Rondnina, M. V., Savelsbergh, A., Katunin, V. I. & Wintermeyer, W. Nature 385, 37-41 (1997); Rodnina, M. V., et al., Proc. Natl. Acad. Sci. USA 96, 9586-9590 (1999)). Therefore, according to the model in Fig. 5, thiostreptone and viomycin must inhibit the translocation of the RRF bound to the A site to the P site. If so, the release of transfer RNA from the P site and E site that must have occurred along with the translocation and further the process of release of the termination complex by the RRF must be inhibited. Accordingly, whether or not the dissociation process of termination complex is inhibited or not in the presence of thiostreptone or viomycin was examined by use of the amount of transfer RNA released from ribosome and the amount of ribosome released from messenger RNA as indices.

The release of transfer RNA from ribosome was examined in the same manner as in Example 4 except that thiostreptone (produced by Sigma Co.) or viomycin (produced by ICN Co.) was added in place of the amidoglycosides. Thiostreptomycin or viomycin was added in an amount of 100  $\mu$ M or 200  $\mu$ M, respectively. The results are shown in Fig. 6.

Also, the release of ribosome from messenger RNA was examined in the same manner as in Example 4 except that thiostreptone or

viomycin was added in place of the amidoglycosides and that in the case where thiostreptone was added, DMSO was added to 0.06% in reaction compounds. Thiostreptomycin or viomycin was added in an amount of 20  $\mu$ M or 50  $\mu$ M, respectively. The results are shown in Table 7.

From Fig. 6, it can be seen that in the presence of thiostreptone or viomycin, the release of transfer RNA was inhibited to a value identical to that of the negative control. Also, from Table 7, it can be seen that in the presence of thiostreptone or viomycin, the release of ribosome was completely inhibited. These results strongly suggest that the translocation of the RRF bound to the A site to the P site is necessary for the expression of the activity of RRF. Therefore, it can be considered that the substance that inhibits the translocation of the RRF can be a potent candidate of an RRF inhibitor.

Example 6. Inhibition of termination complex release by GMPPCP and fusidic acid

It has been known that GMPPCP and fusidic acid are both EFG inhibitors and inhibits the release of termination complex by fixing EFG to ribosome after the translocation of transfer RNA while allow the occurrence of translocation of transfer RNA only once (Inoue-Yokosawa, N., Ishikawa, C. & Kaziro, Y., J. Biol. Chem. 249, 4321-4323 (1974); Rodnina, M. V., Savelsbergh, A., Katunin, V. I. & Wintermeyer, W., Nature, 385, 37-41 (1997); Bodley, J. W., Zieve,

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F. J., Lin, L., & Zieve, S. T., J. Biol. Chem., 245, 5656-5661 (1970); Kuriki, Y., Inoue, N. & Karizo, Y., Biochim. Biophys. Acta, 224, 487-497 (1970)). Therefore, according to the model in Fig. 5, GMPPCP and fusidic acid allow the translocation of the RRF bound to the A site to the P site, so that they must not inhibit the release of transfer RNA from the P site and E site that takes place along with the translocation. On the other hand, since GMPPCP and fusidic acid inhibit the release of termination complex, they must inhibit the release of ribosome from messenger RNA. Accordingly, whether or not the release of transfer RNA from ribosome and release of ribosome from messenger RNA are inhibited or not in the presence of GMPPCP or fusidic acid was examined.

The release of transfer RNA from ribosome was examined in the same manner as in Example 4 except that GMPPCP or fusidic acid was added in place of the amidoglycosides and that in the case where GMPPCP was added, the experiment was performed in the absence of GTP. GMPPCP or fusidic acid was added in an amount of 370  $\mu$ M or 200  $\mu$ M, respectively. The results are shown in Fig. 6.

Also, the release of ribosome from messenger RNA was examined in the same manner as in Example 4 except that GMPPCP (produced by Sigma Co.) or fusidic acid (produced by ICN Co.) was added in place of the amidoglycosides and that in the case where GMPPCP was added, the experiment was performed in the absence of GTP. GMPPCP or fusidic acid was added in an amount of 370  $\mu$ M or 200  $\mu$ M, respectively.

The results are shown in Table 7.

From Fig. 6, it can be seen that even when GMPPCP or fusidic acid was added, the release of transfer RNA was at a value identical to that of the positive control, so that the release of transfer RNA is not inhibited. On the other hand, from Table 7, it can be seen that GMPPCP or fusidic acid completely inhibits the release of ribosome (Igarashi, K., Ishitsuka, H. & Kaji, A., Biochim. Biophys. Res. Commun., 37, 499-504 (1969); Hirashima, A. & Kaji, A., J. Mol. Biol., 65, 43-58 (1972); Ogawa, K. & Kaji, A., Eur. J. Biochem., 58, 411-419 (1975); Karimi, R., Pavlov, M. Y., Buckingham, R. H. & Ehrenberg, M., Molecular cell, 3, 601-609 (1999)).

These results more strongly suggest the possibility that the RRF expresses termination complex release activity by showing a similar behavior to that of transfer RNA and furthermore, the fact that the release of transfer RNA and the release of ribosome can be separately inhibited supports the model shown in Fig. 5 in which the release of termination complex proceeds stepwise by the EFG and RRF.

Example 7. Inhibition of RRF activity by the presence of excessive deacylating transfer RNA

It was strongly suggested by example 4 that it is necessary that the RRF binds to the A site of ribosome for the expression of the activity of the RRF. Accordingly, if excess of transfer RNA

exists, RRF and transfer RNA competitively bind to the A site of ribosome and as a result the dissociation of termination complex will must be inhibited. To confirm this point, inhibition of dissociation of termination complex in the presence of varied concentration of transfer RNA was examined.

Polysome (0.5 to 1 A<sub>260</sub> unit) was incubated in the presence of varied amounts between 0 and 1,000 pmole of RRF, EFG, and GTP, and a varied amount between 0 and 10 nmole of transfer RNA. Then, after performing sucrose density gradient centrifugation (density gradient: 15 to 30%), absorbance at 254 nm was measured to thereby measure the amount of free ribosome. The graph by Lineweavwe-Burk plot prepared on the basis of the measurement results is shown in Fig. 7. The vertical axis represents a reciprocal of the percentage of the amount of free ribosome in the presence of a varied amount of transfer RNA to the amount of free ribosome in the absence of transfer RNA.

In the graph in Fig. 7, the vertical intercept is constant regardless of the amount of transfer RNA and K<sub>m</sub> increases as the amount of transfer RNA increases, so that it can be seen that transfer RNA competitively inhibits the activity of RRF.

Example 8. Inhibition by paromomycin of binding of RRF to ribosome

On the basis of the results in Example 4 and Example 7, the following experiments were performed in order to directly confirm

that paromomycin used in Example 4 inhibits binding of RRF to ribosome.

First, less than 1 pmole of  $^{35}\text{S}$  labeled histidine tagged RRF ( $^{35}\text{S}$ -His-RRF) was incubated in a buffer solution (50 mM Tris-Cl, pH 7.6, 10 mM magnesium acetate, 30 mM potassium chloride, and 1 mM DTT) in the presence of 10 pmole of washed ribosome and a varied concentration of paromomycin at 30 °C for 10 minutes. After removing free  $^{35}\text{S}$ -His-RRF by microconcentration, the amount of ribosome-bound  $^{35}\text{S}$ -His-RRF was measured by radioactivity. The  $^{35}\text{S}$ -His-RRF was prepared by purifying in vitro His-RRF expressed by in the presence of  $^{35}\text{S}$ -labeled methionine by use of  $\text{Ni}^{2+}$  beads. The results are shown in Fig. 8. The binding ratio of RRF is a value calculated by taking the amount of RRF bound to ribosome in the absence of paromomycin as 100%.

From Fig. 8, it can be seen that the binding ratio of RRF decreases depending on the concentration of paromomycin. Therefore, paromomycin is considered to inhibit the activity of RRF by inhibiting the binding of the RRF to ribosome.

Table 8

## Structure cooordinates of RRF

<u>ATOM</u>	<u>Type</u>	<u>Residue</u>	<u>#</u>	<u>X</u>	<u>Y</u>	<u>Z</u>	<u>OCC</u>	<u>B</u>
ATOM	1	CB	VAL	2	10.355	24.444	73.500	1.00 50.36
ATOM	2	CG1	VAL	2	11.185	25.300	72.669	1.00 50.36
ATOM	3	CG2	VAL	2	9.102	25.267	74.125	1.00 50.36
ATOM	4	C	VAL	2	8.502	23.777	72.304	1.00 83.11
ATOM	5	O	VAL	2	8.267	24.906	71.890	1.00 83.11
ATOM	6	N	VAL	2	10.415	23.206	71.242	1.00 83.11
ATOM	7	CA	VAL	2	9.881	23.282	72.625	1.00 83.11
ATOM	8	N	ASN	3	7.567	22.901	72.348	1.00 72.42
ATOM	9	CA	ASN	3	6.364	23.543	72.193	1.00 72.42
ATOM	10	CB	ASN	3	5.458	22.851	71.191	1.00 77.31
ATOM	11	CG	ASN	3	4.541	23.842	70.630	1.00 77.31
ATOM	12	OD1	ASN	3	3.368	23.859	70.934	1.00 77.31
ATOM	13	ND2	ASN	3	5.109	24.802	69.910	1.00 77.31
ATOM	14	C	ASN	3	6.085	23.280	73.622	1.00 72.42
ATOM	15	O	ASN	3	6.652	22.357	74.186	1.00 72.42
ATOM	16	N	PRO	4	5.407	24.244	74.267	1.00 41.97
ATOM	17	CD	PRO	4	4.846	25.501	73.729	1.00 61.56
ATOM	18	CA	PRO	4	5.121	24.010	75.681	1.00 41.97
ATOM	19	CB	PRO	4	3.981	24.999	75.973	1.00 61.56
ATOM	20	CG	PRO	4	3.931	25.973	74.808	1.00 61.56
ATOM	21	C	PRO	4	4.632	22.521	75.634	1.00 41.97

ATOM	22	O	PRO	4	4.781	21.774	76.617	1.00	41.97
ATOM	23	N	PHE	5	4.080	22.114	74.491	1.00	37.43
ATOM	24	CA	PHE	5	3.593	20.751	74.270	1.00	37.43
ATOM	25	CB	PHE	5	2.898	20.648	72.912	1.00	36.55
ATOM	26	CG	PHE	5	1.608	21.414	72.832	1.00	36.55
ATOM	27	CD1	PHE	5	1.285	22.160	71.693	1.00	36.55
ATOM	28	CD2	PHE	5	0.697	21.370	73.868	1.00	36.55
ATOM	29	CE1	PHE	5	0.081	22.866	71.612	1.00	36.55
ATOM	30	CE2	PHE	5	-0.505	22.072	73.792	1.00	36.55
ATOM	31	CZ	PHE	5	-0.815	22.815	72.652	1.00	36.55
ATOM	32	C	PHE	5	4.720	19.724	74.322	1.00	37.43
ATOM	33	O	PHE	5	4.603	18.687	74.974	1.00	37.43
ATOM	34	N	ILE	6	5.812	19.998	73.620	1.00	41.88
ATOM	35	CA	ILE	6	6.946	19.073	73.616	1.00	41.88
ATOM	36	CB	ILE	6	7.997	19.477	72.561	1.00	41.38
ATOM	37	CG2	ILE	6	9.276	18.658	72.740	1.00	41.38
ATOM	38	CG1	ILE	6	7.410	19.266	71.162	1.00	41.38
ATOM	39	CD1	ILE	6	8.209	19.943	70.059	1.00	41.38
ATOM	40	C	ILE	6	7.585	19.045	74.997	1.00	41.88
ATOM	41	O	ILE	6	7.926	17.982	75.516	1.00	41.88
ATOM	42	N	LYS	7	7.738	20.222	75.592	1.00	47.17
ATOM	43	CA	LYS	7	8.309	20.333	76.923	1.00	47.17
ATOM	44	CB	LYS	7	8.293	21.792	77.371	1.00	68.01
ATOM	45	CG	LYS	7	8.925	22.024	78.727	1.00	68.01

ATOM	46	CD	LYS	7	8.706	23.444	79.215	1.00	68.01
ATOM	47	CE	LYS	7	9.525	23.709	80.466	1.00	68.01
ATOM	48	NZ	LYS	7	8.752	24.480	81.480	1.00	68.01
ATOM	49	C	LYS	7	7.451	19.496	77.872	1.00	47.17
ATOM	50	O	LYS	7	7.963	18.740	78.701	1.00	47.17
ATOM	51	N	GLU	8	6.137	19.639	77.732	1.00	39.77
ATOM	52	CA	GLU	8	5.175	18.920	78.555	1.00	39.77
ATOM	53	CB	GLU	8	3.758	19.392	78.230	1.00	50.17
ATOM	54	CG	GLU	8	2.678	18.705	79.047	1.00	50.17
ATOM	55	CD	GLU	8	1.291	18.857	78.443	1.00	50.17
ATOM	56	OE1	GLU	8	0.319	18.370	79.058	1.00	50.17
ATOM	57	OE2	GLU	8	1.170	19.456	77.351	1.00	50.17
ATOM	58	C	GLU	8	5.269	17.406	78.349	1.00	39.77
ATOM	59	O	GLU	8	5.227	16.637	79.311	1.00	39.77
ATOM	60	N	ALA	9	5.385	16.979	77.095	1.00	39.35
ATOM	61	CA	ALA	9	5.487	15.558	76.790	1.00	39.35
ATOM	62	CB	ALA	9	5.452	15.336	75.294	1.00	32.04
ATOM	63	C	ALA	9	6.764	14.965	77.375	1.00	39.35
ATOM	64	O	ALA	9	6.751	13.859	77.905	1.00	39.35
ATOM	65	N	LYS	10	7.872	15.690	77.285	1.00	37.72
ATOM	66	CA	LYS	10	9.120	15.182	77.840	1.00	37.72
ATOM	67	CB	LYS	10	10.277	16.113	77.514	1.00	61.11
ATOM	68	CG	LYS	10	10.990	15.829	76.231	1.00	61.11
ATOM	69	CD	LYS	10	12.171	16.770	76.124	1.00	61.11

ATOM	70	CE	LYS	10	12.574	17.020	74.678	1.00	61.11
ATOM	71	NZ	LYS	10	13.323	18.307	74.569	1.00	61.11
ATOM	72	C	LYS	10	9.037	15.051	79.358	1.00	37.72
ATOM	73	O	LYS	10	9.508	14.073	79.939	1.00	37.72
ATOM	74	N	GLU	11	8.462	16.064	79.996	1.00	33.88
ATOM	75	CA	GLU	11	8.310	16.076	81.445	1.00	33.88
ATOM	76	CB	GLU	11	7.601	17.353	81.879	1.00	67.13
ATOM	77	CG	GLU	11	8.505	18.337	82.587	1.00	67.13
ATOM	78	CD	GLU	11	8.166	19.783	82.266	1.00	67.13
ATOM	79	OE1	GLU	11	6.969	20.147	82.296	1.00	67.13
ATOM	80	OE2	GLU	11	9.107	20.558	81.989	1.00	67.13
ATOM	81	C	GLU	11	7.529	14.860	81.929	1.00	33.88
ATOM	82	O	GLU	11	7.989	14.119	82.792	1.00	33.88
ATOM	83	N	LYS	12	6.349	14.648	81.365	1.00	39.27
ATOM	84	CA	LYS	12	5.528	13.518	81.766	1.00	39.27
ATOM	85	CB	LYS	12	4.137	13.637	81.143	1.00	39.81
ATOM	86	CG	LYS	12	3.424	14.898	81.559	1.00	39.81
ATOM	87	CD	LYS	12	2.028	14.985	80.996	1.00	39.81
ATOM	88	CE	LYS	12	1.299	16.195	81.576	1.00	39.81
ATOM	89	NZ	LYS	12	-0.138	16.215	81.177	1.00	39.81
ATOM	90	C	LYS	12	6.140	12.168	81.415	1.00	39.27
ATOM	91	O	LYS	12	6.132	11.245	82.230	1.00	39.27
ATOM	92	N	MET	13	6.680	12.054	80.206	1.00	33.90
ATOM	93	CA	MET	13	7.278	10.794	79.780	1.00	33.90

	ATOM	94	CB	MET	13	7.651	10.852	78.307	1.00	28.84
	ATOM	95	CG	MET	13	6.478	10.988	77.344	1.00	28.84
	ATOM	96	SD	MET	13	6.965	10.623	75.666	1.00	28.84
	ATOM	97	CE	MET	13	5.331	10.780	74.827	1.00	28.84
	ATOM	98	C	MET	13	8.508	10.455	80.620	1.00	33.90
	ATOM	99	O	MET	13	8.751	9.289	80.918	1.00	33.90
	ATOM	100	N	LYS	14	9.266	11.468	81.007	1.00	36.32
	ATOM	101	CA	LYS	14	10.454	11.270	81.829	1.00	36.32
	ATOM	102	CB	LYS	14	11.207	12.592	81.957	1.00	65.45
	ATOM	103	CG	LYS	14	12.582	12.500	82.550	1.00	65.45
	ATOM	104	CD	LYS	14	12.746	13.568	83.609	1.00	65.45
	ATOM	105	CE	LYS	14	14.212	13.894	83.838	1.00	65.45
	ATOM	106	NZ	LYS	14	14.426	14.645	85.109	1.00	65.45
	ATOM	107	C	LYS	14	10.008	10.798	83.206	1.00	36.32
	ATOM	108	O	LYS	14	10.636	9.943	83.824	1.00	36.32
	ATOM	109	N	ARG	15	8.911	11.358	83.681	1.00	38.00
	ATOM	110	CA	ARG	15	8.416	10.992	84.979	1.00	38.00
	ATOM	111	CB	ARG	15	7.311	11.927	85.390	1.00	88.37
	ATOM	112	CG	ARG	15	7.456	12.225	86.815	1.00	88.37
	ATOM	113	CD	ARG	15	6.197	11.885	87.496	1.00	88.37
	ATOM	114	NE	ARG	15	5.468	13.131	87.703	1.00	88.37
	ATOM	115	CZ	ARG	15	4.230	13.240	88.152	1.00	88.37
	ATOM	116	NH1	ARG	15	3.586	12.163	88.540	1.00	88.37
	ATOM	117	NH2	ARG	15	3.650	14.435	88.213	1.00	88.37

ATOM	118	C	ARG	15	7.932	9.557	85.018	1.00	38.00
ATOM	119	O	ARG	15	8.193	8.825	85.982	1.00	38.00
ATOM	120	N	THR	16	7.236	9.156	83.963	1.00	33.54
ATOM	121	CA	THR	16	6.738	7.794	83.844	1.00	33.54
ATOM	122	CB	THR	16	6.013	7.603	82.499	1.00	26.11
ATOM	123	OG1	THR	16	4.716	8.216	82.562	1.00	26.11
ATOM	124	CG2	THR	16	5.899	6.117	82.148	1.00	26.11
ATOM	125	C	THR	16	7.931	6.841	83.902	1.00	33.54
ATOM	126	O	THR	16	7.956	5.911	84.704	1.00	33.54
ATOM	127	N	LEU	17	8.932	7.102	83.067	1.00	33.14
ATOM	128	CA	LEU	17	10.119	6.269	83.019	1.00	33.14
ATOM	129	CB	LEU	17	11.101	6.824	81.990	1.00	34.14
ATOM	130	CG	LEU	17	12.339	5.962	81.742	1.00	34.14
ATOM	131	CD1	LEU	17	11.951	4.644	81.086	1.00	34.14
ATOM	132	CD2	LEU	17	13.301	6.728	80.857	1.00	34.14
ATOM	133	C	LEU	17	10.783	6.171	84.390	1.00	33.14
ATOM	134	O	LEU	17	11.261	5.107	84.779	1.00	33.14
ATOM	135	N	GLU	18	10.802	7.268	85.135	1.00	32.45
ATOM	136	CA	GLU	18	11.419	7.237	86.454	1.00	32.45
ATOM	137	CB	GLU	18	11.607	8.661	86.990	1.00	59.96
ATOM	138	CG	GLU	18	12.984	9.224	86.630	1.00	59.96
ATOM	139	CD	GLU	18	13.076	10.747	86.698	1.00	59.96
ATOM	140	OE1	GLU	18	12.049	11.401	86.979	1.00	59.96
ATOM	141	OE2	GLU	18	14.185	11.287	86.460	1.00	59.96

ATOM	142	C	GLU	18	10.617	6.370	87.427	1.00	32.45
ATOM	143	O	GLU	18	11.190	5.687	88.282	1.00	32.45
ATOM	144	N	LYS	19	9.295	6.370	87.279	1.00	28.05
ATOM	145	CA	LYS	19	8.453	5.563	88.149	1.00	28.05
ATOM	146	CB	LYS	19	6.976	5.900	87.953	1.00	77.52
ATOM	147	CG	LYS	19	6.557	7.201	88.607	1.00	77.52
ATOM	148	CD	LYS	19	5.099	7.151	89.044	1.00	77.52
ATOM	149	CE	LYS	19	4.700	8.412	89.804	1.00	77.52
ATOM	150	NZ	LYS	19	3.354	8.277	90.440	1.00	77.52
ATOM	151	C	LYS	19	8.673	4.085	87.883	1.00	28.05
ATOM	152	O	LYS	19	8.729	3.275	88.813	1.00	28.05
ATOM	153	N	ILE	20	8.797	3.732	86.608	1.00	37.89
ATOM	154	CA	ILE	20	9.015	2.343	86.236	1.00	37.89
ATOM	155	CB	ILE	20	9.029	2.170	84.707	1.00	33.33
ATOM	156	CG2	ILE	20	9.407	0.744	84.348	1.00	33.33
ATOM	157	CG1	ILE	20	7.665	2.572	84.131	1.00	33.33
ATOM	158	CD1	ILE	20	6.488	1.863	84.752	1.00	33.33
ATOM	159	C	ILE	20	10.339	1.851	86.799	1.00	37.89
ATOM	160	O	ILE	20	10.406	0.793	87.421	1.00	37.89
ATOM	161	N	GLU	21	11.392	2.628	86.583	1.00	35.03
ATOM	162	CA	GLU	21	12.708	2.250	87.075	1.00	35.03
ATOM	163	CB	GLU	21	13.729	3.337	86.732	1.00	30.62
ATOM	164	CG	GLU	21	13.803	3.617	85.237	1.00	30.62
ATOM	165	CD	GLU	21	14.648	4.828	84.908	1.00	30.62

	ATOM	166	OE1	GLU	21	14.706	5.755	85.736	1.00	30.62
	ATOM	167	OE2	GLU	21	15.239	4.866	83.815	1.00	30.62
	ATOM	168	C	GLU	21	12.628	2.055	88.578	1.00	35.03
	ATOM	169	O	GLU	21	13.327	1.228	89.154	1.00	35.03
	ATOM	170	N	ASP	22	11.746	2.821	89.206	1.00	38.35
	ATOM	171	CA	ASP	22	11.560	2.756	90.643	1.00	38.35
	ATOM	172	CB	ASP	22	10.706	3.946	91.088	1.00	38.81
	ATOM	173	CG	ASP	22	10.825	4.230	92.567	1.00	38.81
	ATOM	174	OD1	ASP	22	11.961	4.281	93.066	1.00	38.81
	ATOM	175	OD2	ASP	22	9.784	4.416	93.230	1.00	38.81
	ATOM	176	C	ASP	22	10.888	1.427	90.999	1.00	38.35
	ATOM	177	O	ASP	22	11.355	0.698	91.875	1.00	38.35
	ATOM	178	N	GLU	23	9.804	1.104	90.302	1.00	29.14
	ATOM	179	CA	GLU	23	9.094	-0.142	90.546	1.00	29.14
	ATOM	180	CB	GLU	23	7.875	-0.235	89.633	1.00	47.44
	ATOM	181	CG	GLU	23	6.846	0.839	89.933	1.00	47.44
	ATOM	182	CD	GLU	23	5.624	0.775	89.039	1.00	47.44
	ATOM	183	OE1	GLU	23	4.619	1.425	89.368	1.00	47.44
	ATOM	184	OE2	GLU	23	5.654	0.085	88.005	1.00	47.44
	ATOM	185	C	GLU	23	10.008	-1.349	90.338	1.00	29.14
	ATOM	186	O	GLU	23	10.007	-2.283	91.142	1.00	29.14
	ATOM	187	N	LEU	24	10.796	-1.327	89.266	1.00	38.04
	ATOM	188	CA	LEU	24	11.716	-2.423	88.981	1.00	38.04
	ATOM	189	CB	LEU	24	12.360	-2.229	87.614	1.00	26.06

	ATOM	190	CG	LEU	24	11.366	-2.262	86.456	1.00	26.06
	ATOM	191	CD1	LEU	24	12.097	-1.999	85.165	1.00	26.06
	ATOM	192	CD2	LEU	24	10.657	-3.604	86.415	1.00	26.06
	ATOM	193	C	LEU	24	12.805	-2.520	90.039	1.00	38.04
	ATOM	194	O	LEU	24	13.360	-3.586	90.288	1.00	38.04
	ATOM	195	N	ARG	25	13.097	-1.393	90.666	1.00	38.24
	ATOM	196	CA	ARG	25	14.117	-1.324	91.690	1.00	38.24
	ATOM	197	CB	ARG	25	14.552	0.128	91.846	1.00	32.35
	ATOM	198	CG	ARG	25	15.401	0.400	93.059	1.00	32.35
	ATOM	199	CD	ARG	25	15.612	1.890	93.266	1.00	32.35
	ATOM	200	NE	ARG	25	15.485	2.205	94.680	1.00	32.35
	ATOM	201	CZ	ARG	25	14.386	2.692	95.246	1.00	32.35
	ATOM	202	NH1	ARG	25	13.310	2.945	94.516	1.00	32.35
	ATOM	203	NH2	ARG	25	14.352	2.872	96.557	1.00	32.35
	ATOM	204	C	ARG	25	13.648	-1.884	93.036	1.00	38.24
	ATOM	205	O	ARG	25	14.452	-2.427	93.795	1.00	38.24
	ATOM	206	N	LYS	26	12.352	-1.762	93.323	1.00	37.23
	ATOM	207	CA	LYS	26	11.792	-2.239	94.590	1.00	37.23
	ATOM	208	CB	LYS	26	10.685	-1.287	95.047	1.00	39.64
	ATOM	209	CG	LYS	26	11.150	0.165	95.116	1.00	39.64
	ATOM	210	CD	LYS	26	10.163	1.079	95.826	1.00	39.64
	ATOM	211	CE	LYS	26	8.877	1.234	95.054	1.00	39.64
	ATOM	212	NZ	LYS	26	8.005	2.257	95.699	1.00	39.64
	ATOM	213	C	LYS	26	11.258	-3.672	94.522	1.00	37.23

ATOM	214	O	LYS	26	10.856	-4.257	95.529	1.00	37.23
ATOM	215	N	MET	27	11.270	-4.218	93.318	1.00	33.15
ATOM	216	CA	MET	27	10.814	-5.566	93.008	1.00	33.15
ATOM	217	CB	MET	27	11.078	-5.799	91.535	1.00	37.03
ATOM	218	CG	MET	27	9.999	-6.456	90.761	1.00	37.03
ATOM	219	SD	MET	27	10.710	-6.822	89.162	1.00	37.03
ATOM	220	CE	MET	27	10.529	-8.604	89.133	1.00	37.03
ATOM	221	C	MET	27	11.586	-6.625	93.797	1.00	33.15
ATOM	222	O	MET	27	12.817	-6.535	93.910	1.00	33.15
ATOM	223	N	ARG	28	10.891	-7.632	94.332	1.00	34.95
ATOM	224	CA	ARG	28	11.600	-8.700	95.047	1.00	34.95
ATOM	225	CB	ARG	28	10.653	-9.617	95.831	1.00	37.05
ATOM	226	CG	ARG	28	11.379	-10.784	96.563	1.00	37.05
ATOM	227	CD	ARG	28	11.935	-11.825	95.587	1.00	37.05
ATOM	228	NE	ARG	28	12.853	-12.803	96.172	1.00	37.05
ATOM	229	CZ	ARG	28	12.485	-13.830	96.935	1.00	37.05
ATOM	230	NH1	ARG	28	11.205	-14.023	97.227	1.00	37.05
ATOM	231	NH2	ARG	28	13.397	-14.685	97.381	1.00	37.05
ATOM	232	C	ARG	28	12.284	-9.524	93.976	1.00	34.95
ATOM	233	O	ARG	28	11.663	-9.932	92.999	1.00	34.95
ATOM	234	N	THR	29	13.560	-9.792	94.176	1.00	38.90
ATOM	235	CA	THR	29	14.324	-10.557	93.211	1.00	38.90
ATOM	236	CB	THR	29	15.137	-9.563	92.332	1.00	35.61
ATOM	237	OG1	THR	29	14.492	-9.442	91.059	1.00	35.61

ATOM	238	CG2	THR	29	16.569	-9.974	92.161	1.00	35.61
ATOM	239	C	THR	29	15.184	-11.578	93.952	1.00	38.90
ATOM	240	O	THR	29	15.051	-11.739	95.164	1.00	38.90
ATOM	241	N	GLY	30	16.041	-12.288	93.233	1.00	39.05
ATOM	242	CA	GLY	30	16.877	-13.287	93.870	1.00	39.05
ATOM	243	C	GLY	30	17.824	-12.818	94.961	1.00	39.05
ATOM	244	O	GLY	30	18.097	-13.571	95.894	1.00	39.05
ATOM	245	N	LYS	31	18.327	-11.591	94.864	1.00	44.38
ATOM	246	CA	LYS	31	19.276	-11.095	95.859	1.00	44.38
ATOM	247	CB	LYS	31	20.463	-10.413	95.166	1.00	96.17
ATOM	248	CG	LYS	31	20.425	-8.883	95.169	1.00	96.17
ATOM	249	CD	LYS	31	19.350	-8.309	94.249	1.00	96.17
ATOM	250	CE	LYS	31	19.212	-6.796	94.447	1.00	96.17
ATOM	251	NZ	LYS	31	20.346	-6.211	95.237	1.00	96.17
ATOM	252	C	LYS	31	18.665	-10.138	96.876	1.00	44.38
ATOM	253	O	LYS	31	17.769	-9.360	96.553	1.00	44.38
ATOM	254	N	PRO	32	19.162	-10.176	98.121	1.00	38.22
ATOM	255	CD	PRO	32	20.333	-10.942	98.583	1.00	38.30
ATOM	256	CA	PRO	32	18.663	-9.308	99.190	1.00	38.22
ATOM	257	CB	PRO	32	19.512	-9.720	100.391	1.00	38.30
ATOM	258	CG	PRO	32	20.805	-10.115	99.765	1.00	38.30
ATOM	259	C	PRO	32	18.823	-7.833	98.853	1.00	38.22
ATOM	260	O	PRO	32	19.905	-7.386	98.482	1.00	38.22
ATOM	261	N	SER	33	17.734	-7.082	98.981	1.00	37.83

	ATOM	262	CA	SER	33	17.753	-5.655	98.705	1.00	37.83
	ATOM	263	CB	SER	33	17.385	-5.392	97.245	1.00	42.16
	ATOM	264	OG	SER	33	17.475	-4.009	96.959	1.00	42.16
	ATOM	265	C	SER	33	16.785	-4.914	99.626	1.00	37.83
	ATOM	266	O	SER	33	15.588	-5.189	99.634	1.00	37.83
	ATOM	267	N	PRO	34	17.302	-3.967	100.425	1.00	31.79
	ATOM	268	CD	PRO	34	18.736	-3.767	100.705	1.00	21.38
	ATOM	269	CA	PRO	34	16.450	-3.202	101.343	1.00	31.79
	ATOM	270	CB	PRO	34	17.413	-2.226	102.022	1.00	21.38
	ATOM	271	CG	PRO	34	18.762	-2.426	101.353	1.00	21.38
	ATOM	272	C	PRO	34	15.304	-2.485	100.653	1.00	31.79
	ATOM	273	O	PRO	34	14.306	-2.134	101.285	1.00	31.79
	ATOM	274	N	ALA	35	15.435	-2.301	99.346	1.00	38.20
	ATOM	275	CA	ALA	35	14.432	-1.607	98.561	1.00	38.20
	ATOM	276	CB	ALA	35	14.956	-1.386	97.157	1.00	17.23
	ATOM	277	C	ALA	35	13.072	-2.287	98.506	1.00	38.20
	ATOM	278	O	ALA	35	12.067	-1.630	98.221	1.00	38.20
	ATOM	279	N	ILE	36	13.024	-3.593	98.765	1.00	43.48
	ATOM	280	CA	ILE	36	11.751	-4.315	98.723	1.00	43.48
	ATOM	281	CB	ILE	36	11.950	-5.840	98.563	1.00	35.86
	ATOM	282	CG2	ILE	36	12.611	-6.150	97.237	1.00	35.86
	ATOM	283	CG1	ILE	36	12.815	-6.383	99.691	1.00	35.86
	ATOM	284	CD1	ILE	36	13.127	-7.851	99.539	1.00	35.86
	ATOM	285	C	ILE	36	10.902	-4.072	99.962	1.00	43.48

ATOM	286	O	ILE	36	9.721	-4.402	99.979	1.00	43.48
ATOM	287	N	LEU	37	11.502	-3.493	100.995	1.00	45.44
ATOM	288	CA	LEU	37	10.775	-3.214	102.222	1.00	45.44
ATOM	289	CB	LEU	37	11.697	-3.364	103.431	1.00	37.85
ATOM	290	CG	LEU	37	12.257	-4.779	103.613	1.00	37.85
ATOM	291	CD1	LEU	37	13.166	-4.833	104.832	1.00	37.85
ATOM	292	CD2	LEU	37	11.108	-5.760	103.761	1.00	37.85
ATOM	293	C	LEU	37	10.169	-1.822	102.205	1.00	45.44
ATOM	294	O	LEU	37	9.378	-1.474	103.075	1.00	45.44
ATOM	295	N	GLU	38	10.533	-1.029	101.206	1.00	35.29
ATOM	296	CA	GLU	38	10.024	0.327	101.086	1.00	35.29
ATOM	297	CB	GLU	38	10.727	1.047	99.938	1.00	35.02
ATOM	298	CG	GLU	38	12.126	1.507	100.291	1.00	35.02
ATOM	299	CD	GLU	38	12.859	2.111	99.118	1.00	35.02
ATOM	300	OE1	GLU	38	12.198	2.705	98.240	1.00	35.02
ATOM	301	OE2	GLU	38	14.103	2.005	99.084	1.00	35.02
ATOM	302	C	GLU	38	8.525	0.376	100.881	1.00	35.29
ATOM	303	O	GLU	38	7.898	1.409	101.088	1.00	35.29
ATOM	304	N	GLU	39	7.940	-0.744	100.485	1.00	43.94
ATOM	305	CA	GLU	39	6.503	-0.787	100.259	1.00	43.94
ATOM	306	CB	GLU	39	6.211	-1.291	98.846	1.00	81.69
ATOM	307	CG	GLU	39	6.456	-0.239	97.771	1.00	81.69
ATOM	308	CD	GLU	39	5.420	0.872	97.802	1.00	81.69
ATOM	309	OE1	GLU	39	4.242	0.586	97.505	1.00	81.69

ATOM	310	OE2	GLU	39	5.777	2.027	98.125	1.00	81.69
ATOM	311	C	GLU	39	5.783	-1.642	101.289	1.00	43.94
ATOM	312	O	GLU	39	4.582	-1.860	101.187	1.00	43.94
ATOM	313	N	ILE	40	6.519	-2.130	102.279	1.00	39.98
ATOM	314	CA	ILE	40	5.914	-2.929	103.332	1.00	39.98
ATOM	315	CB	ILE	40	6.874	-4.032	103.844	1.00	36.67
ATOM	316	CG2	ILE	40	6.193	-4.855	104.920	1.00	36.67
ATOM	317	CG1	ILE	40	7.284	-4.952	102.694	1.00	36.67
ATOM	318	CD1	ILE	40	6.116	-5.618	102.010	1.00	36.67
ATOM	319	C	ILE	40	5.591	-1.969	104.478	1.00	39.98
ATOM	320	O	ILE	40	6.490	-1.467	105.153	1.00	39.98
ATOM	321	N	LYS	41	4.305	-1.705	104.682	1.00	42.16
ATOM	322	CA	LYS	41	3.877	-0.797	105.732	1.00	42.16
ATOM	323	CB	LYS	41	2.794	0.146	105.205	1.00	51.75
ATOM	324	CG	LYS	41	3.189	0.926	103.966	1.00	51.75
ATOM	325	CD	LYS	41	1.962	1.566	103.350	1.00	51.75
ATOM	326	CE	LYS	41	2.274	2.250	102.032	1.00	51.75
ATOM	327	NZ	LYS	41	3.149	3.440	102.204	1.00	51.75
ATOM	328	C	LYS	41	3.346	-1.535	106.954	1.00	42.16
ATOM	329	O	LYS	41	2.775	-2.625	106.861	1.00	42.16
ATOM	330	N	VAL	42	3.527	-0.902	108.104	1.00	36.81
ATOM	331	CA	VAL	42	3.099	-1.440	109.377	1.00	36.81
ATOM	332	CB	VAL	42	4.351	-1.856	110.199	1.00	34.57
ATOM	333	CG1	VAL	42	4.204	-1.477	111.654	1.00	34.57

	ATOM	334	CG2	VAL	42	4.578	-3.349	110.051	1.00	34.57
	ATOM	335	C	VAL	42	2.313	-0.330	110.067	1.00	36.81
	ATOM	336	O	VAL	42	2.684	0.836	109.975	1.00	36.81
	ATOM	337	N	ASP	43	1.218	-0.676	110.734	1.00	42.28
	ATOM	338	CA	ASP	43	0.416	0.329	111.424	1.00	42.28
	ATOM	339	CB	ASP	43	-1.006	-0.189	111.671	1.00	62.32
	ATOM	340	CG	ASP	43	-1.902	0.849	112.335	1.00	62.32
	ATOM	341	OD1	ASP	43	-2.036	1.970	111.797	1.00	62.32
	ATOM	342	OD2	ASP	43	-2.484	0.547	113.398	1.00	62.32
	ATOM	343	C	ASP	43	1.099	0.650	112.743	1.00	42.28
	ATOM	344	O	ASP	43	0.885	-0.027	113.744	1.00	42.28
	ATOM	345	N	TYR	44	1.927	1.686	112.729	1.00	35.94
	ATOM	346	CA	TYR	44	2.673	2.111	113.908	1.00	35.94
	ATOM	347	CB	TYR	44	4.131	2.369	113.524	1.00	28.29
	ATOM	348	CG	TYR	44	5.058	2.554	114.707	1.00	28.29
	ATOM	349	CD1	TYR	44	5.766	3.746	114.883	1.00	28.29
	ATOM	350	CE1	TYR	44	6.611	3.920	115.961	1.00	28.29
	ATOM	351	CD2	TYR	44	5.230	1.533	115.650	1.00	28.29
	ATOM	352	CE2	TYR	44	6.081	1.699	116.738	1.00	28.29
	ATOM	353	CZ	TYR	44	6.769	2.893	116.881	1.00	28.29
	ATOM	354	OH	TYR	44	7.623	3.064	117.938	1.00	28.29
	ATOM	355	C	TYR	44	2.069	3.372	114.511	1.00	35.94
	ATOM	356	O	TYR	44	2.100	4.439	113.898	1.00	35.94
	ATOM	357	N	TYR	45	1.528	3.240	115.718	1.00	38.53

ATOM	358	CA	TYR	45	0.889	4.347	116.424	1.00	38.53
ATOM	359	CB	TYR	45	1.935	5.289	117.025	1.00	41.05
ATOM	360	CG	TYR	45	2.617	4.715	118.244	1.00	41.05
ATOM	361	CD1	TYR	45	3.728	3.879	118.120	1.00	41.05
ATOM	362	CE1	TYR	45	4.337	3.317	119.241	1.00	41.05
ATOM	363	CD2	TYR	45	2.144	4.998	119.532	1.00	41.05
ATOM	364	CE2	TYR	45	2.745	4.438	120.662	1.00	41.05
ATOM	365	CZ	TYR	45	3.851	3.610	120.506	1.00	41.05
ATOM	366	OH	TYR	45	4.461	3.056	121.610	1.00	41.05
ATOM	367	C	TYR	45	-0.086	5.148	115.573	1.00	38.53
ATOM	368	O	TYR	45	0.015	6.370	115.489	1.00	38.53
ATOM	369	N	GLY	46	-1.028	4.449	114.945	1.00	42.43
ATOM	370	CA	GLY	46	-2.034	5.107	114.128	1.00	42.43
ATOM	371	C	GLY	46	-1.673	5.501	112.705	1.00	42.43
ATOM	372	O	GLY	46	-2.542	5.949	111.957	1.00	42.43
ATOM	373	N	VAL	47	-0.416	5.327	112.313	1.00	41.54
ATOM	374	CA	VAL	47	0.010	5.700	110.969	1.00	41.54
ATOM	375	CB	VAL	47	0.992	6.898	111.037	1.00	35.99
ATOM	376	CG1	VAL	47	1.674	7.109	109.689	1.00	35.99
ATOM	377	CG2	VAL	47	0.237	8.148	111.451	1.00	35.99
ATOM	378	C	VAL	47	0.663	4.580	110.155	1.00	41.54
ATOM	379	O	VAL	47	1.623	3.958	110.604	1.00	41.54
ATOM	380	N	PRO	48	0.146	4.309	108.943	1.00	40.25
ATOM	381	CD	PRO	48	-1.000	4.969	108.294	1.00	34.00

ATOM	382	CA	PRO	48	0.709	3.259	108.080	1.00	40.25
ATOM	383	CB	PRO	48	-0.119	3.372	106.804	1.00	34.00
ATOM	384	CG	PRO	48	-1.437	3.928	107.293	1.00	34.00
ATOM	385	C	PRO	48	2.156	3.665	107.849	1.00	40.25
ATOM	386	O	PRO	48	2.420	4.700	107.237	1.00	40.25
ATOM	387	N	THR	49	3.096	2.855	108.316	1.00	32.23
ATOM	388	CA	THR	49	4.495	3.232	108.207	1.00	32.23
ATOM	389	CB	THR	49	5.047	3.475	109.622	1.00	26.24
ATOM	390	OG1	THR	49	4.090	4.237	110.368	1.00	26.24
ATOM	391	CG2	THR	49	6.375	4.212	109.574	1.00	26.24
ATOM	392	C	THR	49	5.434	2.271	107.485	1.00	32.23
ATOM	393	O	THR	49	5.561	1.108	107.867	1.00	32.23
ATOM	394	N	PRO	50	6.086	2.742	106.407	1.00	39.12
ATOM	395	CD	PRO	50	5.650	3.818	105.506	1.00	28.33
ATOM	396	CA	PRO	50	6.999	1.833	105.718	1.00	39.12
ATOM	397	CB	PRO	50	7.593	2.691	104.595	1.00	28.33
ATOM	398	CG	PRO	50	6.843	3.998	104.624	1.00	28.33
ATOM	399	C	PRO	50	8.045	1.349	106.709	1.00	39.12
ATOM	400	O	PRO	50	8.515	2.111	107.545	1.00	39.12
ATOM	401	N	VAL	51	8.404	0.076	106.603	1.00	34.69
ATOM	402	CA	VAL	51	9.356	-0.539	107.511	1.00	34.69
ATOM	403	CB	VAL	51	9.576	-2.006	107.122	1.00	36.79
ATOM	404	CG1	VAL	51	10.622	-2.623	108.005	1.00	36.79
ATOM	405	CG2	VAL	51	8.264	-2.773	107.254	1.00	36.79

	ATOM	406	C	VAL	51	10.714	0.138	107.685	1.00	34.69
	ATOM	407	O	VAL	51	11.158	0.336	108.817	1.00	34.69
	ATOM	408	N	ASN	52	11.375	0.493	106.585	1.00	43.32
	ATOM	409	CA	ASN	52	12.694	1.124	106.670	1.00	43.32
	ATOM	410	CB	ASN	52	13.256	1.391	105.274	1.00	45.16
	ATOM	411	CG	ASN	52	12.336	2.247	104.434	1.00	45.16
	ATOM	412	OD1	ASN	52	11.261	1.808	104.033	1.00	45.16
	ATOM	413	ND2	ASN	52	12.747	3.475	104.172	1.00	45.16
	ATOM	414	C	ASN	52	12.698	2.423	107.458	1.00	43.32
	ATOM	415	O	ASN	52	13.754	3.003	107.684	1.00	43.32
	ATOM	416	N	GLN	53	11.522	2.883	107.868	1.00	41.50
	ATOM	417	CA	GLN	53	11.415	4.120	108.635	1.00	41.50
	ATOM	418	CB	GLN	53	10.109	4.841	108.305	1.00	32.22
	ATOM	419	CG	GLN	53	10.163	5.659	107.035	1.00	32.22
	ATOM	420	CD	GLN	53	8.818	6.244	106.664	1.00	32.22
	ATOM	421	OE1	GLN	53	8.030	6.641	107.531	1.00	32.22
	ATOM	422	NE2	GLN	53	8.551	6.320	105.363	1.00	32.22
	ATOM	423	C	GLN	53	11.465	3.823	110.118	1.00	41.50
	ATOM	424	O	GLN	53	11.719	4.713	110.937	1.00	41.50
	ATOM	425	N	LEU	54	11.230	2.559	110.454	1.00	35.24
	ATOM	426	CA	LEU	54	11.230	2.113	111.842	1.00	35.24
	ATOM	427	CB	LEU	54	9.949	1.328	112.132	1.00	27.96
	ATOM	428	CG	LEU	54	8.637	2.050	111.839	1.00	27.96
	ATOM	429	CD1	LEU	54	7.462	1.130	112.101	1.00	27.96

	ATOM	430	CD2	LEU	54	8.555	3.294	112.702	1.00	27.96
	ATOM	431	C	LEU	54	12.427	1.223	112.144	1.00	35.24
	ATOM	432	O	LEU	54	12.525	0.660	113.238	1.00	35.24
	ATOM	433	N	ALA	55	13.341	1.091	111.188	1.00	26.03
	ATOM	434	CA	ALA	55	14.481	0.218	111.411	1.00	26.03
	ATOM	435	CB	ALA	55	14.038	-1.244	111.294	1.00	26.69
	ATOM	436	C	ALA	55	15.638	0.457	110.479	1.00	26.03
	ATOM	437	O	ALA	55	15.495	1.068	109.422	1.00	26.03
	ATOM	438	N	THR	56	16.798	-0.025	110.897	1.00	37.20
	ATOM	439	CA	THR	56	17.994	0.075	110.087	1.00	37.20
	ATOM	440	CB	THR	56	19.261	0.167	110.946	1.00	41.17
	ATOM	441	OG1	THR	56	19.399	-1.027	111.726	1.00	41.17
	ATOM	442	CG2	THR	56	19.177	1.357	111.879	1.00	41.17
	ATOM	443	C	THR	56	18.009	-1.238	109.317	1.00	37.20
	ATOM	444	O	THR	56	17.785	-2.313	109.890	1.00	37.20
	ATOM	445	N	ILE	57	18.244	-1.160	108.017	1.00	53.27
	ATOM	446	CA	ILE	57	18.268	-2.364	107.214	1.00	53.27
	ATOM	447	CB	ILE	57	17.193	-2.321	106.131	1.00	37.44
	ATOM	448	CG2	ILE	57	17.215	-3.612	105.330	1.00	37.44
	ATOM	449	CG1	ILE	57	15.828	-2.101	106.789	1.00	37.44
	ATOM	450	CD1	ILE	57	14.665	-2.037	105.810	1.00	37.44
	ATOM	451	C	ILE	57	19.632	-2.521	106.579	1.00	53.27
	ATOM	452	O	ILE	57	20.124	-1.626	105.899	1.00	53.27
	ATOM	453	N	SER	58	20.248	-3.668	106.820	1.00	58.33

ATOM	454	CA	SER	58	21.571	-3.954	106.287	1.00	58.33
ATOM	455	CB	SER	58	22.609	-3.776	107.395	1.00	54.61
ATOM	456	OG	SER	58	22.130	-4.320	108.610	1.00	54.61
ATOM	457	C	SER	58	21.619	-5.371	105.735	1.00	58.33
ATOM	458	O	SER	58	20.691	-6.142	105.952	1.00	58.33
ATOM	459	N	ILE	59	22.696	-5.719	105.047	1.00	52.33
ATOM	460	CA	ILE	59	22.809	-7.036	104.463	1.00	52.33
ATOM	461	CB	ILE	59	23.345	-6.880	103.002	1.00	41.35
ATOM	462	CG2	ILE	59	23.395	-8.205	102.308	1.00	41.35
ATOM	463	CG1	ILE	59	22.416	-5.923	102.242	1.00	41.35
ATOM	464	CD1	ILE	59	22.248	-6.171	100.721	1.00	41.35
ATOM	465	C	ILE	59	23.718	-7.878	105.353	1.00	52.33
ATOM	466	O	ILE	59	24.936	-7.696	105.361	1.00	52.33
ATOM	467	N	SER	60	23.109	-8.762	106.143	1.00	60.00
ATOM	468	CA	SER	60	23.886	-9.591	107.064	1.00	60.00
ATOM	469	CB	SER	60	23.010	-10.539	107.912	1.00	60.63
ATOM	470	OG	SER	60	22.600	-11.739	107.279	1.00	60.63
ATOM	471	C	SER	60	24.778	-10.428	106.252	1.00	60.00
ATOM	472	O	SER	60	25.950	-10.189	106.125	1.00	60.00
ATOM	473	N	GLU	61	24.235	-11.488	105.732	1.00	87.30
ATOM	474	CA	GLU	61	25.102	-12.210	104.852	1.00	87.30
ATOM	475	CB	GLU	61	25.179	-13.704	105.187	1.00	88.30
ATOM	476	CG	GLU	61	23.932	-14.400	105.050	1.00	88.30
ATOM	477	CD	GLU	61	24.112	-15.569	104.196	1.00	88.30

ATOM	478	OE1	GLU	61	23.382	-15.647	103.202	1.00	88.30
ATOM	479	OE2	GLU	61	24.982	-16.404	104.514	1.00	88.30
ATOM	480	C	GLU	61	24.601	-11.951	103.471	1.00	87.30
ATOM	481	O	GLU	61	23.600	-11.303	103.276	1.00	87.30
ATOM	482	N	GLU	62	25.450	-12.404	102.552	1.00	61.89
ATOM	483	CA	GLU	62	25.257	-12.362	101.100	1.00	61.89
ATOM	484	CB	GLU	62	26.426	-13.116	100.473	1.00	60.63
ATOM	485	CG	GLU	62	27.704	-12.340	100.884	1.00	60.63
ATOM	486	CD	GLU	62	28.278	-12.647	102.306	1.00	60.63
ATOM	487	OE1	GLU	62	27.634	-13.284	103.188	1.00	60.63
ATOM	488	OE2	GLU	62	29.433	-12.215	102.521	1.00	60.63
ATOM	489	C	GLU	62	23.847	-12.744	100.622	1.00	61.89
ATOM	490	O	GLU	62	23.455	-12.418	99.550	1.00	61.89
ATOM	491	N	ARG	63	23.074	-13.357	101.491	1.00	43.14
ATOM	492	CA	ARG	63	21.691	-13.788	101.154	1.00	43.14
ATOM	493	CB	ARG	63	21.592	-15.314	101.038	1.00	76.81
ATOM	494	CG	ARG	63	22.506	-15.940	100.016	1.00	76.81
ATOM	495	CD	ARG	63	21.645	-16.662	99.020	1.00	76.81
ATOM	496	NE	ARG	63	22.409	-17.245	97.930	1.00	76.81
ATOM	497	CZ	ARG	63	21.892	-17.540	96.743	1.00	76.81
ATOM	498	NH1	ARG	63	20.610	-17.305	96.498	1.00	76.81
ATOM	499	NH2	ARG	63	22.663	-18.049	95.793	1.00	76.81
ATOM	500	C	ARG	63	20.705	-13.359	102.198	1.00	43.14
ATOM	501	O	ARG	63	19.544	-13.764	102.165	1.00	43.14

	ATOM	502	N	THR	64	21.161	-12.500	103.109	1.00	37.34
	ATOM	503	CA	THR	64	20.310	-12.052	104.183	1.00	37.34
	ATOM	504	CB	THR	64	20.799	-12.615	105.553	1.00	39.55
	ATOM	505	OG1	THR	64	20.904	-14.040	105.505	1.00	39.55
	ATOM	506	CG2	THR	64	19.819	-12.237	106.662	1.00	39.55
	ATOM	507	C	THR	64	20.118	-10.553	104.378	1.00	37.34
	ATOM	508	O	THR	64	21.053	-9.760	104.271	1.00	37.34
	ATOM	509	N	LEU	65	18.880	-10.188	104.695	1.00	39.85
	ATOM	510	CA	LEU	65	18.516	-8.812	104.998	1.00	39.85
	ATOM	511	CB	LEU	65	17.236	-8.403	104.271	1.00	33.79
	ATOM	512	CG	LEU	65	17.295	-7.751	102.896	1.00	33.79
	ATOM	513	CD1	LEU	65	15.874	-7.601	102.368	1.00	33.79
	ATOM	514	CD2	LEU	65	17.989	-6.408	102.997	1.00	33.79
	ATOM	515	C	LEU	65	18.225	-8.806	106.489	1.00	39.85
	ATOM	516	O	LEU	65	17.402	-9.585	106.956	1.00	39.85
	ATOM	517	N	VAL	66	18.902	-7.950	107.238	1.00	42.65
	ATOM	518	CA	VAL	66	18.649	-7.864	108.666	1.00	42.65
	ATOM	519	CB	VAL	66	19.958	-7.878	109.478	1.00	46.94
	ATOM	520	CG1	VAL	66	19.654	-7.792	110.951	1.00	46.94
	ATOM	521	CG2	VAL	66	20.718	-9.152	109.203	1.00	46.94
	ATOM	522	C	VAL	66	17.904	-6.558	108.909	1.00	42.65
	ATOM	523	O	VAL	66	18.366	-5.487	108.514	1.00	42.65
	ATOM	524	N	ILE	67	16.740	-6.669	109.543	1.00	31.17
	ATOM	525	CA	ILE	67	15.890	-5.526	109.844	1.00	31.17

ATOM	526	CB	ILE	67	14.441	-5.790	109.421	1.00	22.89
ATOM	527	CG2	ILE	67	13.618	-4.516	109.546	1.00	22.89
ATOM	528	CG1	ILE	67	14.401	-6.336	107.987	1.00	22.89
ATOM	529	CD1	ILE	67	13.024	-6.819	107.571	1.00	22.89
ATOM	530	C	ILE	67	15.888	-5.308	111.345	1.00	31.17
ATOM	531	O	ILE	67	15.204	-6.032	112.073	1.00	31.17
ATOM	532	N	LYS	68	16.639	-4.309	111.806	1.00	42.20
ATOM	533	CA	LYS	68	16.719	-4.005	113.229	1.00	42.20
ATOM	534	CB	LYS	68	18.180	-3.819	113.623	1.00	56.36
ATOM	535	CG	LYS	68	18.405	-3.640	115.105	1.00	56.36
ATOM	536	CD	LYS	68	19.850	-3.923	115.458	1.00	56.36
ATOM	537	CE	LYS	68	20.079	-3.792	116.952	1.00	56.36
ATOM	538	NZ	LYS	68	19.129	-4.626	117.749	1.00	56.36
ATOM	539	C	LYS	68	15.913	-2.768	113.634	1.00	42.20
ATOM	540	O	LYS	68	16.306	-1.636	113.360	1.00	42.20
ATOM	541	N	PRO	69	14.763	-2.970	114.283	1.00	39.13
ATOM	542	CD	PRO	69	14.029	-4.240	114.428	1.00	36.24
ATOM	543	CA	PRO	69	13.936	-1.837	114.709	1.00	39.13
ATOM	544	CB	PRO	69	12.530	-2.410	114.649	1.00	36.24
ATOM	545	CG	PRO	69	12.750	-3.805	115.143	1.00	36.24
ATOM	546	C	PRO	69	14.320	-1.409	116.123	1.00	39.13
ATOM	547	O	PRO	69	14.665	-2.247	116.950	1.00	39.13
ATOM	548	N	TRP	70	14.274	-0.112	116.406	1.00	35.31
ATOM	549	CA	TRP	70	14.625	0.359	117.742	1.00	35.31

ATOM	550	CB	TRP	70	14.990	1.843	117.719	1.00	54.18
ATOM	551	CG	TRP	70	14.618	2.524	116.449	1.00	54.18
ATOM	552	CD2	TRP	70	13.375	3.187	116.177	1.00	54.18
ATOM	553	CE2	TRP	70	13.461	3.663	114.844	1.00	54.18
ATOM	554	CE3	TRP	70	12.220	3.423	116.922	1.00	54.18
ATOM	555	CD1	TRP	70	15.371	2.620	115.312	1.00	54.18
ATOM	556	NE1	TRP	70	14.671	3.305	114.345	1.00	54.18
ATOM	557	CZ2	TRP	70	12.400	4.366	114.251	1.00	54.18
ATOM	558	CZ3	TRP	70	11.174	4.121	116.329	1.00	54.18
ATOM	559	CH2	TRP	70	11.276	4.587	115.003	1.00	54.18
ATOM	560	C	TRP	70	13.477	0.111	118.713	1.00	35.31
ATOM	561	O	TRP	70	13.690	0.011	119.913	1.00	35.31
ATOM	562	N	ASP	71	12.259	0.018	118.194	1.00	38.62
ATOM	563	CA	ASP	71	11.097	-0.252	119.036	1.00	38.62
ATOM	564	CB	ASP	71	9.897	0.580	118.587	1.00	33.95
ATOM	565	CG	ASP	71	8.667	0.323	119.436	1.00	33.95
ATOM	566	OD1	ASP	71	8.604	-0.741	120.086	1.00	33.95
ATOM	567	OD2	ASP	71	7.754	1.174	119.445	1.00	33.95
ATOM	568	C	ASP	71	10.785	-1.740	118.869	1.00	38.62
ATOM	569	O	ASP	71	10.037	-2.142	117.972	1.00	38.62
ATOM	570	N	LYS	72	11.361	-2.553	119.741	1.00	42.47
ATOM	571	CA	LYS	72	11.190	-3.990	119.661	1.00	42.47
ATOM	572	CB	LYS	72	11.903	-4.650	120.843	1.00	41.13
ATOM	573	CG	LYS	72	13.420	-4.457	120.777	1.00	41.13

	ATOM	574	CD	LYS	72	13.964	-5.079	119.500	1.00	41.13
	ATOM	575	CE	LYS	72	15.041	-4.235	118.810	1.00	41.13
	ATOM	576	NZ	LYS	72	16.328	-4.168	119.527	1.00	41.13
	ATOM	577	C	LYS	72	9.774	-4.530	119.516	1.00	42.47
	ATOM	578	O	LYS	72	9.600	-5.690	119.148	1.00	42.47
	ATOM	579	N	SER	73	8.759	-3.719	119.781	1.00	36.48
	ATOM	580	CA	SER	73	7.390	-4.212	119.631	1.00	36.48
	ATOM	581	CB	SER	73	6.401	-3.336	120.403	1.00	49.51
	ATOM	582	OG	SER	73	6.288	-2.045	119.832	1.00	49.51
	ATOM	583	C	SER	73	7.030	-4.206	118.153	1.00	36.48
	ATOM	584	O	SER	73	6.006	-4.745	117.750	1.00	36.48
	ATOM	585	N	VAL	74	7.891	-3.593	117.352	1.00	41.78
	ATOM	586	CA	VAL	74	7.690	-3.487	115.910	1.00	41.78
	ATOM	587	CB	VAL	74	8.562	-2.340	115.332	1.00	35.01
	ATOM	588	CG1	VAL	74	8.640	-2.425	113.811	1.00	35.01
	ATOM	589	CG2	VAL	74	7.982	-1.009	115.754	1.00	35.01
	ATOM	590	C	VAL	74	7.997	-4.791	115.176	1.00	41.78
	ATOM	591	O	VAL	74	7.475	-5.032	114.085	1.00	41.78
	ATOM	592	N	LEU	75	8.842	-5.626	115.778	1.00	35.55
	ATOM	593	CA	LEU	75	9.212	-6.914	115.191	1.00	35.55
	ATOM	594	CB	LEU	75	10.063	-7.707	116.180	1.00	30.58
	ATOM	595	CG	LEU	75	11.420	-7.091	116.509	1.00	30.58
	ATOM	596	CD1	LEU	75	12.024	-7.786	117.707	1.00	30.58
	ATOM	597	CD2	LEU	75	12.338	-7.213	115.288	1.00	30.58

	ATOM	598	C	LEU	75	7.968	-7.725	114.828	1.00	35.55
	ATOM	599	O	LEU	75	7.830	-8.220	113.714	1.00	35.55
	ATOM	600	N	SER	76	7.057	-7.850	115.777	1.00	35.44
	ATOM	601	CA	SER	76	5.843	-8.601	115.540	1.00	35.44
	ATOM	602	CB	SER	76	4.954	-8.545	116.782	1.00	41.93
	ATOM	603	OG	SER	76	3.829	-9.382	116.623	1.00	41.93
	ATOM	604	C	SER	76	5.087	-8.062	114.321	1.00	35.44
	ATOM	605	O	SER	76	4.649	-8.831	113.462	1.00	35.44
	ATOM	606	N	LEU	77	4.951	-6.738	114.251	1.00	39.58
	ATOM	607	CA	LEU	77	4.246	-6.078	113.152	1.00	39.58
	ATOM	608	CB	LEU	77	4.097	-4.577	113.446	1.00	32.60
	ATOM	609	CG	LEU	77	3.248	-4.216	114.681	1.00	32.60
	ATOM	610	CD1	LEU	77	3.301	-2.715	114.936	1.00	32.60
	ATOM	611	CD2	LEU	77	1.808	-4.676	114.476	1.00	32.60
	ATOM	612	C	LEU	77	4.941	-6.277	111.805	1.00	39.58
	ATOM	613	O	LEU	77	4.288	-6.510	110.787	1.00	39.58
	ATOM	614	N	ILE	78	6.263	-6.181	111.792	1.00	38.16
	ATOM	615	CA	ILE	78	6.996	-6.362	110.553	1.00	38.16
	ATOM	616	CB	ILE	78	8.501	-6.146	110.753	1.00	31.39
	ATOM	617	CG2	ILE	78	9.240	-6.525	109.478	1.00	31.39
	ATOM	618	CG1	ILE	78	8.773	-4.691	111.153	1.00	31.39
	ATOM	619	CD1	ILE	78	10.212	-4.413	111.518	1.00	31.39
	ATOM	620	C	ILE	78	6.779	-7.774	110.031	1.00	38.16
	ATOM	621	O	ILE	78	6.590	-7.985	108.833	1.00	38.16

ATOM	622	N	GLU	79	6.802	-8.737	110.942	1.00	34.51
ATOM	623	CA	GLU	79	6.618	-10.136	110.599	1.00	34.51
ATOM	624	CB	GLU	79	6.802	-10.982	111.857	1.00	43.51
ATOM	625	CG	GLU	79	6.587	-12.471	111.665	1.00	43.51
ATOM	626	CD	GLU	79	6.869	-13.261	112.931	1.00	43.51
ATOM	627	OE1	GLU	79	6.782	-14.505	112.889	1.00	43.51
ATOM	628	OE2	GLU	79	7.178	-12.642	113.972	1.00	43.51
ATOM	629	C	GLU	79	5.243	-10.387	109.987	1.00	34.51
ATOM	630	O	GLU	79	5.115	-11.058	108.961	1.00	34.51
ATOM	631	N	LYS	80	4.215	-9.846	110.625	1.00	41.03
ATOM	632	CA	LYS	80	2.845	-9.994	110.153	1.00	41.03
ATOM	633	CB	LYS	80	1.905	-9.247	111.090	1.00	63.82
ATOM	634	CG	LYS	80	0.758	-10.055	111.630	1.00	63.82
ATOM	635	CD	LYS	80	1.056	-10.548	113.035	1.00	63.82
ATOM	636	CE	LYS	80	-0.230	-10.873	113.785	1.00	63.82
ATOM	637	NZ	LYS	80	0.064	-11.206	115.204	1.00	63.82
ATOM	638	C	LYS	80	2.695	-9.401	108.753	1.00	41.03
ATOM	639	O	LYS	80	2.128	-10.022	107.847	1.00	41.03
ATOM	640	N	ALA	81	3.198	-8.177	108.601	1.00	39.91
ATOM	641	CA	ALA	81	3.131	-7.437	107.351	1.00	39.91
ATOM	642	CB	ALA	81	3.738	-6.065	107.535	1.00	28.92
ATOM	643	C	ALA	81	3.831	-8.161	106.216	1.00	39.91
ATOM	644	O	ALA	81	3.358	-8.145	105.077	1.00	39.91
ATOM	645	N	ILE	82	4.966	-8.782	106.516	1.00	31.35

ATOM	646	CA	ILE	82	5.691	-9.509	105.490	1.00	31.35
ATOM	647	CB	ILE	82	7.103	-9.899	105.959	1.00	31.86
ATOM	648	CG2	ILE	82	7.746	-10.830	104.943	1.00	31.86
ATOM	649	CG1	ILE	82	7.948	-8.634	106.151	1.00	31.86
ATOM	650	CD1	ILE	82	9.372	-8.905	106.571	1.00	31.86
ATOM	651	C	ILE	82	4.919	-10.759	105.095	1.00	31.35
ATOM	652	O	ILE	82	4.763	-11.041	103.904	1.00	31.35
ATOM	653	N	ASN	83	4.420	-11.503	106.080	1.00	44.39
ATOM	654	CA	ASN	83	3.660	-12.712	105.778	1.00	44.39
ATOM	655	CB	ASN	83	3.253	-13.449	107.064	1.00	33.35
ATOM	656	CG	ASN	83	4.427	-14.137	107.747	1.00	33.35
ATOM	657	OD1	ASN	83	5.289	-14.727	107.092	1.00	33.35
ATOM	658	ND2	ASN	83	4.454	-14.078	109.075	1.00	33.35
ATOM	659	C	ASN	83	2.411	-12.393	104.949	1.00	44.39
ATOM	660	O	ASN	83	1.936	-13.236	104.186	1.00	44.39
ATOM	661	N	ALA	84	1.888	-11.178	105.086	1.00	41.69
ATOM	662	CA	ALA	84	0.698	-10.777	104.334	1.00	41.69
ATOM	663	CB	ALA	84	-0.061	-9.684	105.090	1.00	35.44
ATOM	664	C	ALA	84	1.026	-10.294	102.919	1.00	41.69
ATOM	665	O	ALA	84	0.147	-10.231	102.059	1.00	41.69
ATOM	666	N	SER	85	2.285	-9.945	102.673	1.00	47.02
ATOM	667	CA	SER	85	2.681	-9.478	101.346	1.00	47.02
ATOM	668	CB	SER	85	3.952	-8.645	101.439	1.00	37.52
ATOM	669	OG	SER	85	5.037	-9.457	101.836	1.00	37.52

ATOM	670	C	SER	85	2.931	-10.663	100.421	1.00	47.02
ATOM	671	O	SER	85	2.773	-11.815	100.820	1.00	47.02
ATOM	672	N	ASP	86	3.330	-10.380	99.188	1.00	55.10
ATOM	673	CA	ASP	86	3.600	-11.438	98.226	1.00	55.10
ATOM	674	CB	ASP	86	2.856	-11.159	96.913	1.00	66.61
ATOM	675	CG	ASP	86	3.232	-9.821	96.292	1.00	66.61
ATOM	676	OD1	ASP	86	4.108	-9.119	96.841	1.00	66.61
ATOM	677	OD2	ASP	86	2.647	-9.468	95.244	1.00	66.61
ATOM	678	C	ASP	86	5.093	-11.593	97.955	1.00	55.10
ATOM	679	O	ASP	86	5.492	-12.136	96.921	1.00	55.10
ATOM	680	N	LEU	87	5.916	-11.127	98.889	1.00	40.02
ATOM	681	CA	LEU	87	7.368	-11.201	98.741	1.00	40.02
ATOM	682	CB	LEU	87	8.056	-10.528	99.931	1.00	53.14
ATOM	683	CG	LEU	87	7.867	-9.019	100.053	1.00	53.14
ATOM	684	CD1	LEU	87	8.549	-8.512	101.314	1.00	53.14
ATOM	685	CD2	LEU	87	8.446	-8.348	98.815	1.00	53.14
ATOM	686	C	LEU	87	7.924	-12.612	98.596	1.00	40.02
ATOM	687	O	LEU	87	8.967	-12.812	97.967	1.00	40.02
ATOM	688	N	GLY	88	7.233	-13.588	99.176	1.00	39.77
ATOM	689	CA	GLY	88	7.722	-14.951	99.109	1.00	39.77
ATOM	690	C	GLY	88	8.924	-15.046	100.028	1.00	39.77
ATOM	691	O	GLY	88	9.905	-15.733	99.740	1.00	39.77
ATOM	692	N	LEU	89	8.848	-14.319	101.138	1.00	36.60
ATOM	693	CA	LEU	89	9.907	-14.303	102.124	1.00	36.60

ATOM	694	CB	LEU	89	10.522	-12.909	102.221	1.00	41.00
ATOM	695	CG	LEU	89	11.343	-12.412	101.033	1.00	41.00
ATOM	696	CD1	LEU	89	11.804	-10.996	101.312	1.00	41.00
ATOM	697	CD2	LEU	89	12.539	-13.321	100.797	1.00	41.00
ATOM	698	C	LEU	89	9.348	-14.720	103.477	1.00	36.60
ATOM	699	O	LEU	89	8.186	-14.464	103.792	1.00	36.60
ATOM	700	N	ASN	90	10.185	-15.368	104.275	1.00	32.75
ATOM	701	CA	ASN	90	9.774	-15.834	105.585	1.00	32.75
ATOM	702	CB	ASN	90	9.973	-17.343	105.682	1.00	37.39
ATOM	703	CG	ASN	90	9.128	-18.104	104.682	1.00	37.39
ATOM	704	OD1	ASN	90	7.902	-18.176	104.813	1.00	37.39
ATOM	705	ND2	ASN	90	9.776	-18.671	103.670	1.00	37.39
ATOM	706	C	ASN	90	10.593	-15.141	106.651	1.00	32.75
ATOM	707	O	ASN	90	11.804	-15.323	106.731	1.00	32.75
ATOM	708	N	PRO	91	9.941	-14.330	107.484	1.00	35.24
ATOM	709	CD	PRO	91	8.503	-14.012	107.514	1.00	26.32
ATOM	710	CA	PRO	91	10.657	-13.620	108.543	1.00	35.24
ATOM	711	CB	PRO	91	9.597	-12.670	109.088	1.00	26.32
ATOM	712	CG	PRO	91	8.339	-13.443	108.899	1.00	26.32
ATOM	713	C	PRO	91	11.212	-14.545	109.621	1.00	35.24
ATOM	714	O	PRO	91	10.577	-15.528	110.004	1.00	35.24
ATOM	715	N	ILE	92	12.406	-14.224	110.099	1.00	39.44
ATOM	716	CA	ILE	92	13.050	-14.988	111.156	1.00	39.44
ATOM	717	CB	ILE	92	14.442	-15.457	110.736	1.00	30.73

ATOM	718	CG2	ILE	92	15.044	-16.318	111.833	1.00	30.73
ATOM	719	CG1	ILE	92	14.357	-16.256	109.440	1.00	30.73
ATOM	720	CD1	ILE	92	15.720	-16.628	108.899	1.00	30.73
ATOM	721	C	ILE	92	13.199	-14.016	112.323	1.00	39.44
ATOM	722	O	ILE	92	14.117	-13.200	112.347	1.00	39.44
ATOM	723	N	ASN	93	12.291	-14.109	113.287	1.00	37.86
ATOM	724	CA	ASN	93	12.275	-13.220	114.441	1.00	37.86
ATOM	725	CB	ASN	93	10.818	-12.947	114.804	1.00	26.31
ATOM	726	CG	ASN	93	10.660	-11.871	115.856	1.00	26.31
ATOM	727	OD1	ASN	93	11.627	-11.440	116.482	1.00	26.31
ATOM	728	ND2	ASN	93	9.426	-11.431	116.059	1.00	26.31
ATOM	729	C	ASN	93	13.015	-13.760	115.668	1.00	37.86
ATOM	730	O	ASN	93	12.538	-14.690	116.321	1.00	37.86
ATOM	731	N	ASP	94	14.166	-13.174	115.995	1.00	43.86
ATOM	732	CA	ASP	94	14.926	-13.613	117.167	1.00	43.86
ATOM	733	CB	ASP	94	16.429	-13.647	116.866	1.00	48.91
ATOM	734	CG	ASP	94	17.003	-12.274	116.625	1.00	48.91
ATOM	735	OD1	ASP	94	18.236	-12.162	116.455	1.00	48.91
ATOM	736	OD2	ASP	94	16.220	-11.305	116.603	1.00	48.91
ATOM	737	C	ASP	94	14.661	-12.696	118.366	1.00	43.86
ATOM	738	O	ASP	94	15.416	-12.690	119.339	1.00	43.86
ATOM	739	N	GLY	95	13.589	-11.914	118.286	1.00	38.45
ATOM	740	CA	GLY	95	13.233	-11.031	119.381	1.00	38.45
ATOM	741	C	GLY	95	14.025	-9.743	119.451	1.00	38.45

ATOM	742	O	GLY	95	13.756	-8.886	120.293	1.00	38.45
ATOM	743	N	ASN	96	15.008	-9.606	118.569	1.00	49.36
ATOM	744	CA	ASN	96	15.841	-8.410	118.525	1.00	49.36
ATOM	745	CB	ASN	96	17.296	-8.751	118.860	1.00	40.40
ATOM	746	CG	ASN	96	18.208	-7.532	118.808	1.00	40.40
ATOM	747	OD1	ASN	96	19.369	-7.620	118.399	1.00	40.40
ATOM	748	ND2	ASN	96	17.686	-6.388	119.232	1.00	40.40
ATOM	749	C	ASN	96	15.789	-7.849	117.116	1.00	49.36
ATOM	750	O	ASN	96	15.489	-6.679	116.901	1.00	49.36
ATOM	751	N	VAL	97	16.079	-8.716	116.158	1.00	44.00
ATOM	752	CA	VAL	97	16.105	-8.340	114.759	1.00	44.00
ATOM	753	CB	VAL	97	17.561	-8.390	114.253	1.00	36.85
ATOM	754	CG1	VAL	97	17.828	-9.690	113.506	1.00	36.85
ATOM	755	CG2	VAL	97	17.843	-7.197	113.413	1.00	36.85
ATOM	756	C	VAL	97	15.223	-9.276	113.923	1.00	44.00
ATOM	757	O	VAL	97	14.713	-10.279	114.422	1.00	44.00
ATOM	758	N	ILE	98	15.033	-8.938	112.653	1.00	37.43
ATOM	759	CA	ILE	98	14.240	-9.772	111.758	1.00	37.43
ATOM	760	CB	ILE	98	12.936	-9.084	111.332	1.00	38.61
ATOM	761	CG2	ILE	98	12.439	-9.659	110.012	1.00	38.61
ATOM	762	CG1	ILE	98	11.885	-9.281	112.420	1.00	38.61
ATOM	763	CD1	ILE	98	10.495	-8.910	111.987	1.00	38.61
ATOM	764	C	ILE	98	15.036	-10.105	110.515	1.00	37.43
ATOM	765	O	ILE	98	15.270	-9.236	109.677	1.00	37.43

ATOM	766	N	ARG	99	15.458	-11.365	110.410	1.00	30.52
ATOM	767	CA	ARG	99	16.232	-11.822	109.263	1.00	30.52
ATOM	768	CB	ARG	99	17.137	-13.004	109.625	1.00	50.62
ATOM	769	CG	ARG	99	18.429	-12.643	110.328	1.00	50.62
ATOM	770	CD	ARG	99	19.445	-13.758	110.162	1.00	50.62
ATOM	771	NE	ARG	99	18.996	-15.003	110.777	1.00	50.62
ATOM	772	CZ	ARG	99	19.434	-16.213	110.440	1.00	50.62
ATOM	773	NH1	ARG	99	20.340	-16.363	109.479	1.00	50.62
ATOM	774	NH2	ARG	99	18.962	-17.277	111.074	1.00	50.62
ATOM	775	C	ARG	99	15.307	-12.244	108.151	1.00	30.52
ATOM	776	O	ARG	99	14.242	-12.809	108.385	1.00	30.52
ATOM	777	N	LEU	100	15.729	-11.957	106.932	1.00	33.80
ATOM	778	CA	LEU	100	14.973	-12.307	105.743	1.00	33.80
ATOM	779	CB	LEU	100	14.399	-11.042	105.117	1.00	34.63
ATOM	780	CG	LEU	100	12.890	-10.941	104.938	1.00	34.63
ATOM	781	CD1	LEU	100	12.167	-11.437	106.178	1.00	34.63
ATOM	782	CD2	LEU	100	12.542	-9.493	104.636	1.00	34.63
ATOM	783	C	LEU	100	16.011	-12.928	104.829	1.00	33.80
ATOM	784	O	LEU	100	16.829	-12.225	104.247	1.00	33.80
ATOM	785	N	VAL	101	16.006	-14.248	104.725	1.00	40.27
ATOM	786	CA	VAL	101	16.989	-14.911	103.887	1.00	40.27
ATOM	787	CB	VAL	101	17.377	-16.271	104.470	1.00	42.80
ATOM	788	CG1	VAL	101	18.462	-16.902	103.621	1.00	42.80
ATOM	789	CG2	VAL	101	17.867	-16.097	105.888	1.00	42.80

ATOM	790	C	VAL	101	16.481	-15.087	102.467	1.00	40.27
ATOM	791	O	VAL	101	15.288	-15.295	102.248	1.00	40.27
ATOM	792	N	PHE	102	17.396	-14.988	101.506	1.00	42.62
ATOM	793	CA	PHE	102	17.065	-15.120	100.091	1.00	42.62
ATOM	794	CB	PHE	102	17.504	-13.870	99.325	1.00	35.61
ATOM	795	CG	PHE	102	16.807	-12.614	99.755	1.00	35.61
ATOM	796	CD1	PHE	102	17.012	-12.089	101.026	1.00	35.61
ATOM	797	CD2	PHE	102	15.936	-11.955	98.889	1.00	35.61
ATOM	798	CE1	PHE	102	16.365	-10.926	101.427	1.00	35.61
ATOM	799	CE2	PHE	102	15.286	-10.793	99.284	1.00	35.61
ATOM	800	CZ	PHE	102	15.498	-10.280	100.553	1.00	35.61
ATOM	801	C	PHE	102	17.758	-16.330	99.481	1.00	42.62
ATOM	802	O	PHE	102	18.853	-16.210	98.938	1.00	42.62
ATOM	803	N	PRO	103	17.123	-17.509	99.542	1.00	35.91
ATOM	804	CD	PRO	103	15.787	-17.769	100.101	1.00	36.33
ATOM	805	CA	PRO	103	17.710	-18.739	98.983	1.00	35.91
ATOM	806	CB	PRO	103	16.665	-19.811	99.313	1.00	36.33
ATOM	807	CG	PRO	103	15.900	-19.221	100.488	1.00	36.33
ATOM	808	C	PRO	103	17.961	-18.650	97.472	1.00	35.91
ATOM	809	O	PRO	103	17.379	-17.803	96.789	1.00	35.91
ATOM	810	N	SER	104	18.833	-19.516	96.958	1.00	42.91
ATOM	811	CA	SER	104	19.119	-19.556	95.524	1.00	42.91
ATOM	812	CB	SER	104	19.973	-20.773	95.166	1.00	41.87
ATOM	813	OG	SER	104	21.321	-20.599	95.559	1.00	41.87

ATOM	814	C	SER	104	17.779	-19.663	94.820	1.00	42.91
ATOM	815	O	SER	104	16.993	-20.575	95.089	1.00	42.91
ATOM	816	N	PRO	105	17.494	-18.735	93.905	1.00	35.96
ATOM	817	CD	PRO	105	18.214	-17.490	93.571	1.00	31.16
ATOM	818	CA	PRO	105	16.195	-18.829	93.228	1.00	35.96
ATOM	819	CB	PRO	105	16.084	-17.493	92.488	1.00	31.16
ATOM	820	CG	PRO	105	17.542	-17.062	92.303	1.00	31.16
ATOM	821	C	PRO	105	15.989	-20.037	92.322	1.00	35.96
ATOM	822	O	PRO	105	16.929	-20.569	91.726	1.00	35.96
ATOM	823	N	THR	106	14.740	-20.472	92.249	1.00	50.79
ATOM	824	CA	THR	106	14.354	-21.596	91.410	1.00	50.79
ATOM	825	CB	THR	106	13.050	-22.237	91.919	1.00	55.41
ATOM	826	OG1	THR	106	11.965	-21.318	91.742	1.00	55.41
ATOM	827	CG2	THR	106	13.166	-22.582	93.399	1.00	55.41
ATOM	828	C	THR	106	14.110	-21.029	90.015	1.00	50.79
ATOM	829	O	THR	106	13.845	-19.833	89.865	1.00	50.79
ATOM	830	N	THR	107	14.187	-21.871	88.990	1.00	61.13
ATOM	831	CA	THR	107	13.973	-21.366	87.643	1.00	61.13
ATOM	832	CB	THR	107	14.421	-22.403	86.562	1.00	71.51
ATOM	833	OG1	THR	107	15.405	-21.800	85.707	1.00	71.51
ATOM	834	CG2	THR	107	13.244	-22.863	85.713	1.00	71.51
ATOM	835	C	THR	107	12.515	-20.960	87.454	1.00	61.13
ATOM	836	O	THR	107	12.166	-20.321	86.471	1.00	61.13
ATOM	837	N	GLU	108	11.663	-21.311	88.405	1.00	63.04

ATOM	838	CA	GLU	108	10.262	-20.940	88.297	1.00	63.04
ATOM	839	CB	GLU	108	9.377	-21.956	89.023	1.00	93.70
ATOM	840	CG	GLU	108	8.021	-22.149	88.359	1.00	93.70
ATOM	841	CD	GLU	108	7.250	-23.329	88.922	1.00	93.70
ATOM	842	OE1	GLU	108	6.636	-23.184	90.001	1.00	93.70
ATOM	843	OE2	GLU	108	7.266	-24.406	88.286	1.00	93.70
ATOM	844	C	GLU	108	10.077	-19.544	88.891	1.00	63.04
ATOM	845	O	GLU	108	9.144	-18.822	88.526	1.00	63.04
ATOM	846	N	GLN	109	10.968	-19.173	89.808	1.00	42.84
ATOM	847	CA	GLN	109	10.924	-17.854	90.429	1.00	42.84
ATOM	848	CB	GLN	109	11.763	-17.824	91.710	1.00	42.35
ATOM	849	CG	GLN	109	11.132	-18.557	92.890	1.00	42.35
ATOM	850	CD	GLN	109	11.971	-18.472	94.156	1.00	42.35
ATOM	851	OE1	GLN	109	13.094	-18.964	94.204	1.00	42.35
ATOM	852	NE2	GLN	109	11.423	-17.842	95.186	1.00	42.35
ATOM	853	C	GLN	109	11.473	-16.836	89.434	1.00	42.84
ATOM	854	O	GLN	109	10.866	-15.794	89.200	1.00	42.84
ATOM	855	N	ARG	110	12.624	-17.148	88.846	1.00	37.85
ATOM	856	CA	ARG	110	13.237	-16.258	87.873	1.00	37.85
ATOM	857	CB	ARG	110	14.464	-16.909	87.244	1.00	51.08
ATOM	858	CG	ARG	110	15.598	-17.191	88.202	1.00	51.08
ATOM	859	CD	ARG	110	16.692	-17.973	87.495	1.00	51.08
ATOM	860	NE	ARG	110	17.755	-18.390	88.405	1.00	51.08
ATOM	861	CZ	ARG	110	18.663	-17.569	88.927	1.00	51.08

ATOM	862	NH1	ARG	110	18.644	-16.275	88.629	1.00	51.08
ATOM	863	NH2	ARG	110	19.592	-18.042	89.751	1.00	51.08
ATOM	864	C	ARG	110	12.224	-15.946	86.783	1.00	37.85
ATOM	865	O	ARG	110	11.986	-14.782	86.457	1.00	37.85
ATOM	866	N	ALA	111	11.623	-16.992	86.224	1.00	49.18
ATOM	867	CA	ALA	111	10.634	-16.817	85.168	1.00	49.18
ATOM	868	CB	ALA	111	10.130	-18.172	84.682	1.00	35.40
ATOM	869	C	ALA	111	9.473	-15.978	85.689	1.00	49.18
ATOM	870	O	ALA	111	8.913	-15.158	84.961	1.00	49.18
ATOM	871	N	LYS	112	9.119	-16.175	86.954	1.00	39.11
ATOM	872	CA	LYS	112	8.023	-15.416	87.545	1.00	39.11
ATOM	873	CB	LYS	112	7.687	-15.945	88.940	1.00	85.43
ATOM	874	CG	LYS	112	6.573	-15.162	89.618	1.00	85.43
ATOM	875	CD	LYS	112	6.468	-15.473	91.105	1.00	85.43
ATOM	876	CE	LYS	112	5.400	-14.606	91.768	1.00	85.43
ATOM	877	NZ	LYS	112	5.303	-14.821	93.242	1.00	85.43
ATOM	878	C	LYS	112	8.380	-13.936	87.642	1.00	39.11
ATOM	879	O	LYS	112	7.586	-13.076	87.268	1.00	39.11
ATOM	880	N	TRP	113	9.578	-13.649	88.146	1.00	31.83
ATOM	881	CA	TRP	113	10.042	-12.274	88.299	1.00	31.83
ATOM	882	CB	TRP	113	11.368	-12.237	89.075	1.00	25.54
ATOM	883	CG	TRP	113	11.256	-12.810	90.459	1.00	25.54
ATOM	884	CD2	TRP	113	12.278	-13.490	91.203	1.00	25.54
ATOM	885	CE2	TRP	113	11.711	-13.879	92.434	1.00	25.54

ATOM	886	CE3	TRP	113	13.618	-13.816	90.945	1.00	25.54
ATOM	887	CD1	TRP	113	10.149	-12.803	91.253	1.00	25.54
ATOM	888	NE1	TRP	113	10.411	-13.443	92.439	1.00	25.54
ATOM	889	CZ2	TRP	113	12.434	-14.574	93.412	1.00	25.54
ATOM	890	CZ3	TRP	113	14.342	-14.510	91.927	1.00	25.54
ATOM	891	CH2	TRP	113	13.744	-14.881	93.140	1.00	25.54
ATOM	892	C	TRP	113	10.202	-11.542	86.966	1.00	31.83
ATOM	893	O	TRP	113	9.883	-10.362	86.868	1.00	31.83
ATOM	894	N	VAL	114	10.694	-12.235	85.944	1.00	37.08
ATOM	895	CA	VAL	114	10.873	-11.619	84.631	1.00	37.08
ATOM	896	CB	VAL	114	11.568	-12.588	83.636	1.00	25.80
ATOM	897	CG1	VAL	114	11.544	-12.001	82.229	1.00	25.80
ATOM	898	CG2	VAL	114	13.006	-12.844	84.067	1.00	25.80
ATOM	899	C	VAL	114	9.504	-11.247	84.078	1.00	37.08
ATOM	900	O	VAL	114	9.323	-10.198	83.456	1.00	37.08
ATOM	901	N	LYS	115	8.540	-12.122	84.314	1.00	37.76
ATOM	902	CA	LYS	115	7.177	-11.911	83.861	1.00	37.76
ATOM	903	CB	LYS	115	6.345	-13.151	84.189	1.00	60.43
ATOM	904	CG	LYS	115	5.206	-13.437	83.232	1.00	60.43
ATOM	905	CD	LYS	115	3.844	-13.292	83.904	1.00	60.43
ATOM	906	CE	LYS	115	2.935	-14.479	83.591	1.00	60.43
ATOM	907	NZ	LYS	115	1.512	-14.209	83.953	1.00	60.43
ATOM	908	C	LYS	115	6.613	-10.682	84.580	1.00	37.76
ATOM	909	O	LYS	115	5.863	-9.895	83.999	1.00	37.76

	ATOM	910	N	LYS	116	6.988	-10.519	85.847	1.00	44.68
	ATOM	911	CA	LYS	116	6.528	-9.392	86.649	1.00	44.68
	ATOM	912	CB	LYS	116	6.848	-9.639	88.124	1.00	47.83
	ATOM	913	CG	LYS	116	6.427	-8.510	89.052	1.00	47.83
	ATOM	914	CD	LYS	116	6.846	-8.804	90.480	1.00	47.83
	ATOM	915	CE	LYS	116	6.582	-7.623	91.400	1.00	47.83
	ATOM	916	NZ	LYS	116	7.136	-7.862	92.768	1.00	47.83
	ATOM	917	C	LYS	116	7.174	-8.081	86.184	1.00	44.68
	ATOM	918	O	LYS	116	6.527	-7.029	86.162	1.00	44.68
	ATOM	919	N	ALA	117	8.450	-8.142	85.816	1.00	31.99
	ATOM	920	CA	ALA	117	9.152	-6.959	85.345	1.00	31.99
	ATOM	921	CB	ALA	117	10.615	-7.272	85.121	1.00	21.76
	ATOM	922	C	ALA	117	8.525	-6.491	84.043	1.00	31.99
	ATOM	923	O	ALA	117	8.311	-5.302	83.832	1.00	31.99
	ATOM	924	N	LYS	118	8.222	-7.443	83.173	1.00	40.71
	ATOM	925	CA	LYS	118	7.632	-7.137	81.883	1.00	40.71
	ATOM	926	CB	LYS	118	7.499	-8.421	81.063	1.00	61.77
	ATOM	927	CG	LYS	118	7.281	-8.200	79.577	1.00	61.77
	ATOM	928	CD	LYS	118	7.510	-9.495	78.812	1.00	61.77
	ATOM	929	CE	LYS	118	7.974	-9.237	77.381	1.00	61.77
	ATOM	930	NZ	LYS	118	8.495	-10.490	76.749	1.00	61.77
	ATOM	931	C	LYS	118	6.271	-6.474	82.027	1.00	40.71
	ATOM	932	O	LYS	118	5.953	-5.529	81.312	1.00	40.71
	ATOM	933	N	GLU	119	5.462	-6.956	82.956	1.00	33.86

	ATOM	934	CA	GLU	119	4.140	-6.377	83.111	1.00	33.86
	ATOM	935	CB	GLU	119	3.274	-7.279	83.991	1.00	64.63
	ATOM	936	CG	GLU	119	1.788	-7.224	83.639	1.00	64.63
	ATOM	937	CD	GLU	119	1.530	-7.160	82.133	1.00	64.63
	ATOM	938	OE1	GLU	119	0.818	-6.227	81.703	1.00	64.63
	ATOM	939	OE2	GLU	119	2.032	-8.028	81.381	1.00	64.63
	ATOM	940	C	GLU	119	4.245	-4.962	83.674	1.00	33.86
	ATOM	941	O	GLU	119	3.429	-4.095	83.362	1.00	33.86
	ATOM	942	N	ILE	120	5.270	-4.730	84.487	1.00	30.00
	ATOM	943	CA	ILE	120	5.500	-3.420	85.063	1.00	30.00
	ATOM	944	CB	ILE	120	6.656	-3.458	86.100	1.00	30.15
	ATOM	945	CG2	ILE	120	7.168	-2.049	86.372	1.00	30.15
	ATOM	946	CG1	ILE	120	6.176	-4.116	87.398	1.00	30.15
	ATOM	947	CD1	ILE	120	7.292	-4.435	88.385	1.00	30.15
	ATOM	948	C	ILE	120	5.882	-2.461	83.935	1.00	30.00
	ATOM	949	O	ILE	120	5.408	-1.325	83.882	1.00	30.00
	ATOM	950	N	VAL	121	6.741	-2.927	83.035	1.00	35.95
	ATOM	951	CA	VAL	121	7.188	-2.105	81.923	1.00	35.95
	ATOM	952	CB	VAL	121	8.459	-2.707	81.278	1.00	26.65
	ATOM	953	CG1	VAL	121	8.765	-2.014	79.968	1.00	26.65
	ATOM	954	CG2	VAL	121	9.636	-2.547	82.230	1.00	26.65
	ATOM	955	C	VAL	121	6.094	-1.913	80.869	1.00	35.95
	ATOM	956	O	VAL	121	6.014	-0.854	80.230	1.00	35.95
	ATOM	957	N	GLU	122	5.261	-2.934	80.674	1.00	34.93

	ATOM	958	CA	GLU	122	4.169	-2.822	79.718	1.00	34.93
	ATOM	959	CB	GLU	122	3.357	-4.114	79.647	1.00	40.08
	ATOM	960	CG	GLU	122	3.868	-5.140	78.652	1.00	40.08
	ATOM	961	CD	GLU	122	3.852	-4.634	77.226	1.00	40.08
	ATOM	962	OE1	GLU	122	4.946	-4.398	76.666	1.00	40.08
	ATOM	963	OE2	GLU	122	2.747	-4.469	76.667	1.00	40.08
	ATOM	964	C	GLU	122	3.260	-1.697	80.191	1.00	34.93
	ATOM	965	O	GLU	122	2.807	-0.877	79.397	1.00	34.93
	ATOM	966	N	GLU	123	2.992	-1.665	81.491	1.00	32.96
	ATOM	967	CA	GLU	123	2.138	-0.630	82.043	1.00	32.96
	ATOM	968	CB	GLU	123	1.928	-0.843	83.547	1.00	59.85
	ATOM	969	CG	GLU	123	0.992	-1.999	83.912	1.00	59.85
	ATOM	970	CD	GLU	123	-0.405	-1.850	83.318	1.00	59.85
	ATOM	971	OE1	GLU	123	-0.950	-0.726	83.334	1.00	59.85
	ATOM	972	OE2	GLU	123	-0.970	-2.860	82.843	1.00	59.85
	ATOM	973	C	GLU	123	2.732	0.753	81.785	1.00	32.96
	ATOM	974	O	GLU	123	2.006	1.695	81.462	1.00	32.96
	ATOM	975	N	GLY	124	4.052	0.870	81.920	1.00	39.02
	ATOM	976	CA	GLY	124	4.707	2.147	81.690	1.00	39.02
	ATOM	977	C	GLY	124	4.549	2.599	80.249	1.00	39.02
	ATOM	978	O	GLY	124	4.365	3.783	79.972	1.00	39.02
	ATOM	979	N	LYS	125	4.620	1.643	79.328	1.00	35.24
	ATOM	980	CA	LYS	125	4.474	1.925	77.909	1.00	35.24
	ATOM	981	CB	LYS	125	4.620	0.661	77.098	1.00	34.74

	ATOM	982	CG	LYS	125	5.913	-0.048	77.285	1.00	34.74
	ATOM	983	CD	LYS	125	5.958	-1.196	76.321	1.00	34.74
	ATOM	984	CE	LYS	125	7.363	-1.576	76.003	1.00	34.74
	ATOM	985	NZ	LYS	125	7.313	-2.617	74.961	1.00	34.74
	ATOM	986	C	LYS	125	3.097	2.466	77.638	1.00	35.24
	ATOM	987	O	LYS	125	2.926	3.440	76.893	1.00	35.24
	ATOM	988	N	ILE	126	2.104	1.794	78.215	1.00	32.74
Q	ATOM	989	CA	ILE	126	0.725	2.208	78.047	1.00	32.74
Q	ATOM	990	CB	ILE	126	-0.219	1.320	78.864	1.00	29.38
Q	ATOM	991	CG2	ILE	126	-1.642	1.859	78.801	1.00	29.38
Q	ATOM	992	CG1	ILE	126	-0.154	-0.112	78.335	1.00	29.38
Q	ATOM	993	CD1	ILE	126	-1.019	-1.088	79.110	1.00	29.38
Q	ATOM	994	C	ILE	126	0.628	3.650	78.522	1.00	32.74
Q	ATOM	995	O	ILE	126	-0.019	4.475	77.885	1.00	32.74
Q	ATOM	996	N	ALA	127	1.302	3.956	79.626	1.00	29.45
Q	ATOM	997	CA	ALA	127	1.284	5.309	80.166	1.00	29.45
Q	ATOM	998	CB	ALA	127	2.028	5.356	81.501	1.00	24.11
Q	ATOM	999	C	ALA	127	1.922	6.273	79.170	1.00	29.45
Q	ATOM	1000	O	ALA	127	1.434	7.386	78.978	1.00	29.45
Q	ATOM	1001	N	ILE	128	3.013	5.847	78.536	1.00	32.93
Q	ATOM	1002	CA	ILE	128	3.691	6.687	77.552	1.00	32.93
Q	ATOM	1003	CB	ILE	128	4.936	5.983	76.957	1.00	23.94
Q	ATOM	1004	CG2	ILE	128	5.442	6.742	75.725	1.00	23.94
Q	ATOM	1005	CG1	ILE	128	6.031	5.871	78.021	1.00	23.94

ATOM	1006	CD1	ILE	128	6.454	7.190	78.612	1.00	23.94
ATOM	1007	C	ILE	128	2.732	7.015	76.413	1.00	32.93
ATOM	1008	O	ILE	128	2.524	8.173	76.077	1.00	32.93
ATOM	1009	N	ARG	129	2.142	5.985	75.826	1.00	31.09
ATOM	1010	CA	ARG	129	1.221	6.190	74.731	1.00	31.09
ATOM	1011	CB	ARG	129	0.764	4.844	74.183	1.00	31.49
ATOM	1012	CG	ARG	129	1.917	3.977	73.731	1.00	31.49
ATOM	1013	CD	ARG	129	1.471	2.930	72.738	1.00	31.49
ATOM	1014	NE	ARG	129	2.600	2.124	72.292	1.00	31.49
ATOM	1015	CZ	ARG	129	2.977	0.984	72.858	1.00	31.49
ATOM	1016	NH1	ARG	129	2.300	0.510	73.894	1.00	31.49
ATOM	1017	NH2	ARG	129	4.040	0.326	72.396	1.00	31.49
ATOM	1018	C	ARG	129	0.016	7.040	75.110	1.00	31.09
ATOM	1019	O	ARG	129	-0.590	7.665	74.242	1.00	31.09
ATOM	1020	N	ASN	130	-0.348	7.069	76.389	1.00	30.83
ATOM	1021	CA	ASN	130	-1.489	7.881	76.786	1.00	30.83
ATOM	1022	CB	ASN	130	-1.981	7.517	78.193	1.00	39.26
ATOM	1023	CG	ASN	130	-2.935	6.328	78.185	1.00	39.26
ATOM	1024	OD1	ASN	130	-3.616	6.075	77.188	1.00	39.26
ATOM	1025	ND2	ASN	130	-3.005	5.610	79.301	1.00	39.26
ATOM	1026	C	ASN	130	-1.083	9.340	76.732	1.00	30.83
ATOM	1027	O	ASN	130	-1.826	10.185	76.230	1.00	30.83
ATOM	1028	N	ILE	131	0.108	9.627	77.247	1.00	30.20
ATOM	1029	CA	ILE	131	0.635	10.981	77.229	1.00	30.20

	ATOM	1030	CB	ILE	131	2.061	11.008	77.807	1.00	27.12
	ATOM	1031	CG2	ILE	131	2.740	12.339	77.485	1.00	27.12
	ATOM	1032	CG1	ILE	131	2.003	10.728	79.310	1.00	27.12
	ATOM	1033	CD1	ILE	131	3.357	10.540	79.955	1.00	27.12
	ATOM	1034	C	ILE	131	0.655	11.475	75.780	1.00	30.20
	ATOM	1035	O	ILE	131	0.271	12.607	75.493	1.00	30.20
	ATOM	1036	N	ARG	132	1.094	10.610	74.869	1.00	30.22
G	ATOM	1037	CA	ARG	132	1.149	10.943	73.452	1.00	30.22
G	ATOM	1038	CB	ARG	132	1.653	9.744	72.649	1.00	38.82
G	ATOM	1039	CG	ARG	132	1.395	9.844	71.152	1.00	38.82
G	ATOM	1040	CD	ARG	132	1.837	8.584	70.433	1.00	38.82
G	ATOM	1041	NE	ARG	132	1.578	8.664	69.003	1.00	38.82
G	ATOM	1042	CZ	ARG	132	0.370	8.586	68.441	1.00	38.82
G	ATOM	1043	NH1	ARG	132	-0.718	8.412	69.185	1.00	38.82
G	ATOM	1044	NH2	ARG	132	0.245	8.714	67.125	1.00	38.82
G	ATOM	1045	C	ARG	132	-0.221	11.359	72.926	1.00	30.22
G	ATOM	1046	O	ARG	132	-0.356	12.389	72.271	1.00	30.22
G	ATOM	1047	N	ARG	133	-1.236	10.549	73.213	1.00	41.63
G	ATOM	1048	CA	ARG	133	-2.593	10.829	72.757	1.00	41.63
G	ATOM	1049	CB	ARG	133	-3.498	9.635	73.059	1.00	50.13
G	ATOM	1050	CG	ARG	133	-4.978	9.972	73.139	1.00	50.13
G	ATOM	1051	CD	ARG	133	-5.837	8.757	72.843	1.00	50.13
G	ATOM	1052	NE	ARG	133	-5.188	7.531	73.287	1.00	50.13
G	ATOM	1053	CZ	ARG	133	-5.005	7.195	74.560	1.00	50.13

ATOM	1054	NH1	ARG	133	-5.432	7.992	75.537	1.00	50.13
ATOM	1055	NH2	ARG	133	-4.373	6.066	74.854	1.00	50.13
ATOM	1056	C	ARG	133	-3.209	12.105	73.328	1.00	41.63
ATOM	1057	O	ARG	133	-3.878	12.844	72.611	1.00	41.63
ATOM	1058	N	GLU	134	-2.989	12.366	74.612	1.00	37.67
ATOM	1059	CA	GLU	134	-3.550	13.559	75.234	1.00	37.67
ATOM	1060	CB	GLU	134	-3.257	13.580	76.738	1.00	95.55
ATOM	1061	CG	GLU	134	-1.777	13.566	77.082	1.00	95.55
ATOM	1062	CD	GLU	134	-1.425	14.478	78.245	1.00	95.55
ATOM	1063	OE1	GLU	134	-0.804	13.991	79.218	1.00	95.55
ATOM	1064	OE2	GLU	134	-1.763	15.682	78.179	1.00	95.55
ATOM	1065	C	GLU	134	-2.996	14.826	74.594	1.00	37.67
ATOM	1066	O	GLU	134	-3.747	15.736	74.254	1.00	37.67
ATOM	1067	N	ILE	135	-1.678	14.874	74.431	1.00	35.92
ATOM	1068	CA	ILE	135	-1.016	16.031	73.850	1.00	35.92
ATOM	1069	CB	ILE	135	0.513	15.905	73.985	1.00	39.63
ATOM	1070	CG2	ILE	135	1.200	17.111	73.381	1.00	39.63
ATOM	1071	CG1	ILE	135	0.875	15.794	75.464	1.00	39.63
ATOM	1072	CD1	ILE	135	2.359	15.720	75.741	1.00	39.63
ATOM	1073	C	ILE	135	-1.382	16.183	72.386	1.00	35.92
ATOM	1074	O	ILE	135	-1.687	17.281	71.920	1.00	35.92
ATOM	1075	N	LEU	136	-1.354	15.072	71.665	1.00	41.46
ATOM	1076	CA	LEU	136	-1.682	15.081	70.254	1.00	41.46
ATOM	1077	CB	LEU	136	-1.679	13.655	69.711	1.00	34.36

ATOM	1078	CG	LEU	136	-0.757	13.364	68.526	1.00	34.36
ATOM	1079	CD1	LEU	136	0.525	14.169	68.631	1.00	34.36
ATOM	1080	CD2	LEU	136	-0.460	11.869	68.494	1.00	34.36
ATOM	1081	C	LEU	136	-3.030	15.745	70.004	1.00	41.46
ATOM	1082	O	LEU	136	-3.172	16.506	69.056	1.00	41.46
ATOM	1083	N	LYS	137	-4.020	15.484	70.850	1.00	45.83
ATOM	1084	CA	LYS	137	-5.318	16.109	70.634	1.00	45.83
ATOM	1085	CB	LYS	137	-6.449	15.330	71.326	1.00	74.57
ATOM	1086	CG	LYS	137	-6.404	15.320	72.835	1.00	74.57
ATOM	1087	CD	LYS	137	-7.364	14.283	73.409	1.00	74.57
ATOM	1088	CE	LYS	137	-8.739	14.854	73.707	1.00	74.57
ATOM	1089	NZ	LYS	137	-9.587	13.839	74.405	1.00	74.57
ATOM	1090	C	LYS	137	-5.311	17.559	71.087	1.00	45.83
ATOM	1091	O	LYS	137	-6.112	18.355	70.611	1.00	45.83
ATOM	1092	N	LYS	138	-4.421	17.911	72.008	1.00	38.48
ATOM	1093	CA	LYS	138	-4.343	19.298	72.434	1.00	38.48
ATOM	1094	CB	LYS	138	-3.485	19.450	73.689	1.00	46.05
ATOM	1095	CG	LYS	138	-4.322	19.614	74.943	1.00	46.05
ATOM	1096	CD	LYS	138	-3.486	19.890	76.177	1.00	46.05
ATOM	1097	CE	LYS	138	-2.736	18.654	76.639	1.00	46.05
ATOM	1098	NZ	LYS	138	-2.026	18.906	77.934	1.00	46.05
ATOM	1099	C	LYS	138	-3.751	20.104	71.278	1.00	38.48
ATOM	1100	O	LYS	138	-4.104	21.266	71.070	1.00	38.48
ATOM	1101	N	ILE	139	-2.859	19.476	70.518	1.00	31.21

ATOM	1102	CA	ILE	139	-2.255	20.128	69.366	1.00	31.21
ATOM	1103	CB	ILE	139	-1.038	19.329	68.845	1.00	30.83
ATOM	1104	CG2	ILE	139	-0.604	19.859	67.490	1.00	30.83
ATOM	1105	CG1	ILE	139	0.124	19.430	69.840	1.00	30.83
ATOM	1106	CD1	ILE	139	1.240	18.448	69.571	1.00	30.83
ATOM	1107	C	ILE	139	-3.311	20.222	68.264	1.00	31.21
ATOM	1108	O	ILE	139	-3.432	21.249	67.600	1.00	31.21
ATOM	1109	N	LYS	140	-4.077	19.147	68.081	1.00	37.01
ATOM	1110	CA	LYS	140	-5.129	19.105	67.068	1.00	37.01
ATOM	1111	CB	LYS	140	-5.858	17.765	67.111	1.00	60.99
ATOM	1112	CG	LYS	140	-6.134	17.149	65.751	1.00	60.99
ATOM	1113	CD	LYS	140	-4.888	16.462	65.195	1.00	60.99
ATOM	1114	CE	LYS	140	-5.206	15.633	63.949	1.00	60.99
ATOM	1115	NZ	LYS	140	-4.049	14.793	63.505	1.00	60.99
ATOM	1116	C	LYS	140	-6.136	20.223	67.322	1.00	37.01
ATOM	1117	O	LYS	140	-6.665	20.828	66.383	1.00	37.01
ATOM	1118	N	GLU	141	-6.402	20.485	68.599	1.00	32.47
ATOM	1119	CA	GLU	141	-7.335	21.527	68.994	1.00	32.47
ATOM	1120	CB	GLU	141	-7.497	21.545	70.512	1.00	56.18
ATOM	1121	CG	GLU	141	-8.789	20.933	71.011	1.00	56.18
ATOM	1122	CD	GLU	141	-8.646	20.300	72.394	1.00	56.18
ATOM	1123	OE1	GLU	141	-8.088	20.951	73.310	1.00	56.18
ATOM	1124	OE2	GLU	141	-9.102	19.146	72.562	1.00	56.18
ATOM	1125	C	GLU	141	-6.797	22.862	68.527	1.00	32.47

	ATOM	1126	O	GLU	141	-7.491	23.630	67.860	1.00	32.47
	ATOM	1127	N	ASP	142	-5.548	23.135	68.887	1.00	43.49
	ATOM	1128	CA	ASP	142	-4.911	24.379	68.504	1.00	43.49
	ATOM	1129	CB	ASP	142	-3.510	24.449	69.105	1.00	40.36
	ATOM	1130	CG	ASP	142	-3.523	24.880	70.557	1.00	40.36
	ATOM	1131	OD1	ASP	142	-4.599	24.852	71.180	1.00	40.36
	ATOM	1132	OD2	ASP	142	-2.455	25.246	71.082	1.00	40.36
	ATOM	1133	C	ASP	142	-4.860	24.497	66.987	1.00	43.49
	ATOM	1134	O	ASP	142	-5.002	25.592	66.443	1.00	43.49
	ATOM	1135	N	GLN	143	-4.667	23.374	66.302	1.00	38.41
	ATOM	1136	CA	GLN	143	-4.634	23.401	64.848	1.00	38.41
	ATOM	1137	CB	GLN	143	-4.197	22.045	64.270	1.00	36.16
	ATOM	1138	CG	GLN	143	-4.584	21.868	62.799	1.00	36.16
	ATOM	1139	CD	GLN	143	-4.063	20.585	62.152	1.00	36.16
	ATOM	1140	OE1	GLN	143	-3.863	19.562	62.814	1.00	36.16
	ATOM	1141	NE2	GLN	143	-3.869	20.632	60.843	1.00	36.16
	ATOM	1142	C	GLN	143	-6.025	23.757	64.329	1.00	38.41
	ATOM	1143	O	GLN	143	-6.161	24.502	63.362	1.00	38.41
	ATOM	1144	N	LYS	144	-7.060	23.238	64.981	1.00	41.80
	ATOM	1145	CA	LYS	144	-8.428	23.511	64.549	1.00	41.80
	ATOM	1146	CB	LYS	144	-9.405	22.591	65.283	1.00	70.22
	ATOM	1147	CG	LYS	144	-10.807	22.637	64.711	1.00	70.22
	ATOM	1148	CD	LYS	144	-11.689	21.509	65.226	1.00	70.22
	ATOM	1149	CE	LYS	144	-13.040	21.518	64.514	1.00	70.22

	ATOM	1150	NZ	LYS	144	-13.922	20.387	64.915	1.00	70.22
	ATOM	1151	C	LYS	144	-8.840	24.982	64.730	1.00	41.80
	ATOM	1152	O	LYS	144	-9.540	25.542	63.885	1.00	41.80
	ATOM	1153	N	GLU	145	-8.404	25.616	65.814	1.00	32.59
	ATOM	1154	CA	GLU	145	-8.753	27.020	66.029	1.00	32.59
	ATOM	1155	CB	GLU	145	-8.406	27.480	67.435	1.00	54.82
	ATOM	1156	CG	GLU	145	-8.937	26.652	68.554	1.00	54.82
	ATOM	1157	CD	GLU	145	-8.574	27.273	69.878	1.00	54.82
	ATOM	1158	OE1	GLU	145	-8.448	26.529	70.874	1.00	54.82
	ATOM	1159	OE2	GLU	145	-8.418	28.515	69.915	1.00	54.82
	ATOM	1160	C	GLU	145	-7.997	27.933	65.078	1.00	32.59
	ATOM	1161	O	GLU	145	-8.346	29.108	64.938	1.00	32.59
	ATOM	1162	N	GLY	146	-6.938	27.406	64.463	1.00	27.98
	ATOM	1163	CA	GLY	146	-6.153	28.200	63.539	1.00	27.98
	ATOM	1164	C	GLY	146	-4.874	28.738	64.154	1.00	27.98
	ATOM	1165	O	GLY	146	-4.094	29.421	63.487	1.00	27.98
	ATOM	1166	N	LEU	147	-4.654	28.437	65.429	1.00	31.04
	ATOM	1167	CA	LEU	147	-3.451	28.896	66.108	1.00	31.04
	ATOM	1168	CB	LEU	147	-3.506	28.528	67.590	1.00	33.77
	ATOM	1169	CG	LEU	147	-4.561	29.240	68.439	1.00	33.77
	ATOM	1170	CD1	LEU	147	-4.518	28.698	69.852	1.00	33.77
	ATOM	1171	CD2	LEU	147	-4.293	30.738	68.437	1.00	33.77
	ATOM	1172	C	LEU	147	-2.211	28.269	65.481	1.00	31.04
	ATOM	1173	O	LEU	147	-1.216	28.947	65.227	1.00	31.04

ATOM	1174	N	ILE	148	-2.285	26.965	65.239	1.00	38.27
ATOM	1175	CA	ILE	148	-1.182	26.213	64.658	1.00	38.27
ATOM	1176	CB	ILE	148	-0.917	24.931	65.461	1.00	29.04
ATOM	1177	CG2	ILE	148	0.141	24.102	64.778	1.00	29.04
ATOM	1178	CG1	ILE	148	-0.503	25.287	66.884	1.00	29.04
ATOM	1179	CD1	ILE	148	-0.470	24.104	67.811	1.00	29.04
ATOM	1180	C	ILE	148	-1.517	25.811	63.236	1.00	38.27
ATOM	1181	O	ILE	148	-2.359	24.936	63.021	1.00	38.27
ATOM	1182	N	PRO	149	-0.872	26.446	62.243	1.00	34.71
ATOM	1183	CD	PRO	149	0.123	27.528	62.327	1.00	39.35
ATOM	1184	CA	PRO	149	-1.157	26.094	60.849	1.00	34.71
ATOM	1185	CB	PRO	149	-0.294	27.079	60.053	1.00	39.35
ATOM	1186	CG	PRO	149	0.821	27.421	60.993	1.00	39.35
ATOM	1187	C	PRO	149	-0.806	24.633	60.592	1.00	34.71
ATOM	1188	O	PRO	149	0.086	24.083	61.236	1.00	34.71
ATOM	1189	N	GLU	150	-1.518	24.010	59.657	1.00	45.51
ATOM	1190	CA	GLU	150	-1.319	22.602	59.315	1.00	45.51
ATOM	1191	CB	GLU	150	-1.953	22.304	57.960	1.00	61.98
ATOM	1192	CG	GLU	150	-1.981	20.829	57.631	1.00	61.98
ATOM	1193	CD	GLU	150	-2.892	20.505	56.460	1.00	61.98
ATOM	1194	OE1	GLU	150	-2.978	19.313	56.086	1.00	61.98
ATOM	1195	OE2	GLU	150	-3.524	21.438	55.915	1.00	61.98
ATOM	1196	C	GLU	150	0.127	22.106	59.316	1.00	45.51
ATOM	1197	O	GLU	150	0.452	21.141	60.001	1.00	45.51

	ATOM	1198	N	ASP	151	0.994	22.753	58.549	1.00	41.19
	ATOM	1199	CA	ASP	151	2.392	22.340	58.486	1.00	41.19
	ATOM	1200	CB	ASP	151	3.152	23.242	57.517	1.00	62.06
	ATOM	1201	CG	ASP	151	2.710	23.042	56.088	1.00	62.06
	ATOM	1202	OD1	ASP	151	3.050	23.886	55.232	1.00	62.06
	ATOM	1203	OD2	ASP	151	2.025	22.033	55.817	1.00	62.06
	ATOM	1204	C	ASP	151	3.096	22.322	59.845	1.00	41.19
Q	ATOM	1205	O	ASP	151	3.879	21.416	60.131	1.00	41.19
Q	ATOM	1206	N	ASP	152	2.825	23.316	60.683	1.00	40.51
Q	ATOM	1207	CA	ASP	152	3.461	23.366	61.998	1.00	40.51
Q	ATOM	1208	CB	ASP	152	3.259	24.736	62.642	1.00	57.97
Q	ATOM	1209	CG	ASP	152	3.931	25.841	61.865	1.00	57.97
Q	ATOM	1210	OD1	ASP	152	3.460	26.168	60.760	1.00	57.97
Q	ATOM	1211	OD2	ASP	152	4.942	26.379	62.354	1.00	57.97
Q	ATOM	1212	C	ASP	152	2.908	22.282	62.910	1.00	40.51
Q	ATOM	1213	O	ASP	152	3.598	21.794	63.799	1.00	40.51
Q	ATOM	1214	N	ALA	153	1.656	21.907	62.678	1.00	34.68
Q	ATOM	1215	CA	ALA	153	1.012	20.881	63.472	1.00	34.68
Q	ATOM	1216	CB	ALA	153	-0.485	20.867	63.185	1.00	29.15
Q	ATOM	1217	C	ALA	153	1.633	19.532	63.130	1.00	34.68
Q	ATOM	1218	O	ALA	153	1.885	18.707	64.010	1.00	34.68
Q	ATOM	1219	N	LYS	154	1.895	19.314	61.848	1.00	39.97
Q	ATOM	1220	CA	LYS	154	2.484	18.057	61.424	1.00	39.97
Q	ATOM	1221	CB	LYS	154	2.539	17.971	59.899	1.00	79.16

	ATOM	1222	CG	LYS	154		1.176	17.724	59.270	1.00	79.16
	ATOM	1223	CD	LYS	154		1.238	17.768	57.753	1.00	79.16
	ATOM	1224	CE	LYS	154		-0.150	17.675	57.135	1.00	79.16
	ATOM	1225	NZ	LYS	154		-0.105	17.865	55.654	1.00	79.16
	ATOM	1226	C	LYS	154		3.861	17.813	62.014	1.00	39.97
	ATOM	1227	O	LYS	154		4.124	16.716	62.498	1.00	39.97
	ATOM	1228	N	ARG	155		4.740	18.813	62.005	1.00	39.62
O	ATOM	1229	CA	ARG	155		6.075	18.588	62.560	1.00	39.62
S	ATOM	1230	CB	ARG	155		7.053	19.698	62.160	1.00	60.09
S	ATOM	1231	CG	ARG	155		6.945	20.956	62.975	1.00	60.09
S	ATOM	1232	CD	ARG	155		8.256	21.723	62.990	1.00	60.09
S	ATOM	1233	NE	ARG	155		8.047	23.093	63.448	1.00	60.09
S	ATOM	1234	CZ	ARG	155		7.654	23.432	64.674	1.00	60.09
S	ATOM	1235	NH1	ARG	155		7.434	22.501	65.594	1.00	60.09
S	ATOM	1236	NH2	ARG	155		7.447	24.709	64.972	1.00	60.09
S	ATOM	1237	C	ARG	155		6.028	18.462	64.081	1.00	39.62
S	ATOM	1238	O	ARG	155		6.890	17.831	64.693	1.00	39.62
S	ATOM	1239	N	LEU	156		5.014	19.067	64.686	1.00	37.71
S	ATOM	1240	CA	LEU	156		4.840	19.002	66.131	1.00	37.71
S	ATOM	1241	CB	LEU	156		3.717	19.951	66.556	1.00	41.73
S	ATOM	1242	CG	LEU	156		3.959	20.955	67.691	1.00	41.73
S	ATOM	1243	CD1	LEU	156		5.447	21.194	67.929	1.00	41.73
S	ATOM	1244	CD2	LEU	156		3.258	22.257	67.324	1.00	41.73
S	ATOM	1245	C	LEU	156		4.473	17.558	66.471	1.00	37.71

ATOM	1246	O	LEU	156	4.996	16.982	67.420	1.00	37.71
ATOM	1247	N	GLU	157	3.578	16.981	65.673	1.00	38.40
ATOM	1248	CA	GLU	157	3.140	15.606	65.867	1.00	38.40
ATOM	1249	CB	GLU	157	2.013	15.278	64.885	1.00	42.33
ATOM	1250	CG	GLU	157	0.741	16.056	65.182	1.00	42.33
ATOM	1251	CD	GLU	157	-0.137	16.281	63.961	1.00	42.33
ATOM	1252	OE1	GLU	157	-1.113	17.060	64.072	1.00	42.33
ATOM	1253	OE2	GLU	157	0.145	15.690	62.896	1.00	42.33
ATOM	1254	C	GLU	157	4.312	14.644	65.687	1.00	38.40
ATOM	1255	O	GLU	157	4.451	13.682	66.443	1.00	38.40
ATOM	1256	N	ASN	158	5.157	14.912	64.694	1.00	42.65
ATOM	1257	CA	ASN	158	6.323	14.072	64.437	1.00	42.65
ATOM	1258	CB	ASN	158	7.060	14.549	63.187	1.00	53.78
ATOM	1259	CG	ASN	158	6.273	14.298	61.923	1.00	53.78
ATOM	1260	OD1	ASN	158	6.565	14.868	60.868	1.00	53.78
ATOM	1261	ND2	ASN	158	5.268	13.432	62.016	1.00	53.78
ATOM	1262	C	ASN	158	7.274	14.100	65.627	1.00	42.65
ATOM	1263	O	ASN	158	7.824	13.068	66.021	1.00	42.65
ATOM	1264	N	GLU	159	7.468	15.282	66.203	1.00	41.03
ATOM	1265	CA	GLU	159	8.352	15.400	67.350	1.00	41.03
ATOM	1266	CB	GLU	159	8.517	16.865	67.760	1.00	80.12
ATOM	1267	CG	GLU	159	9.384	17.043	68.999	1.00	80.12
ATOM	1268	CD	GLU	159	10.772	16.430	68.852	1.00	80.12
ATOM	1269	OE1	GLU	159	11.367	16.051	69.889	1.00	80.12

ATOM	1270	OE2	GLU	159	11.270	16.337	67.708	1.00	80.12
ATOM	1271	C	GLU	159	7.803	14.579	68.516	1.00	41.03
ATOM	1272	O	GLU	159	8.551	13.882	69.200	1.00	41.03
ATOM	1273	N	ILE	160	6.496	14.656	68.737	1.00	37.16
ATOM	1274	CA	ILE	160	5.878	13.896	69.810	1.00	37.16
ATOM	1275	CB	ILE	160	4.369	14.254	69.961	1.00	41.43
ATOM	1276	CG2	ILE	160	3.548	13.011	70.247	1.00	41.43
ATOM	1277	CG1	ILE	160	4.173	15.224	71.130	1.00	41.43
ATOM	1278	CD1	ILE	160	4.867	16.538	70.976	1.00	41.43
ATOM	1279	C	ILE	160	6.040	12.413	69.502	1.00	37.16
ATOM	1280	O	ILE	160	6.320	11.607	70.386	1.00	37.16
ATOM	1281	N	GLN	161	5.875	12.056	68.236	1.00	40.44
ATOM	1282	CA	GLN	161	6.007	10.667	67.824	1.00	40.44
ATOM	1283	CB	GLN	161	5.642	10.518	66.348	1.00	47.39
ATOM	1284	CG	GLN	161	5.636	9.082	65.878	1.00	47.39
ATOM	1285	CD	GLN	161	4.721	8.211	66.716	1.00	47.39
ATOM	1286	OE1	GLN	161	5.116	7.136	67.178	1.00	47.39
ATOM	1287	NE2	GLN	161	3.489	8.667	66.914	1.00	47.39
ATOM	1288	C	GLN	161	7.435	10.171	68.064	1.00	40.44
ATOM	1289	O	GLN	161	7.643	9.034	68.498	1.00	40.44
ATOM	1290	N	ALA	162	8.416	11.029	67.785	1.00	32.94
ATOM	1291	CA	ALA	162	9.810	10.670	67.986	1.00	32.94
ATOM	1292	CB	ALA	162	10.719	11.759	67.434	1.00	30.93
ATOM	1293	C	ALA	162	10.056	10.465	69.478	1.00	32.94

ATOM	1294	O	ALA	162	10.733	9.511	69.876	1.00	32.94
ATOM	1295	N	LEU	163	9.492	11.350	70.299	1.00	31.29
ATOM	1296	CA	LEU	163	9.629	11.256	71.759	1.00	31.29
ATOM	1297	CB	LEU	163	8.952	12.438	72.446	1.00	44.08
ATOM	1298	CG	LEU	163	9.756	13.730	72.562	1.00	44.08
ATOM	1299	CD1	LEU	163	8.899	14.794	73.242	1.00	44.08
ATOM	1300	CD2	LEU	163	11.026	13.467	73.362	1.00	44.08
ATOM	1301	C	LEU	163	9.016	9.970	72.298	1.00	31.29
ATOM	1302	O	LEU	163	9.566	9.337	73.197	1.00	31.29
ATOM	1303	N	THR	164	7.867	9.601	71.746	1.00	30.16
ATOM	1304	CA	THR	164	7.175	8.389	72.147	1.00	30.16
ATOM	1305	CB	THR	164	5.812	8.280	71.431	1.00	32.81
ATOM	1306	OG1	THR	164	4.972	9.360	71.849	1.00	32.81
ATOM	1307	CG2	THR	164	5.125	6.972	71.766	1.00	32.81
ATOM	1308	C	THR	164	8.033	7.163	71.825	1.00	30.16
ATOM	1309	O	THR	164	8.212	6.290	72.674	1.00	30.16
ATOM	1310	N	ASP	165	8.567	7.093	70.609	1.00	36.74
ATOM	1311	CA	ASP	165	9.405	5.954	70.237	1.00	36.74
ATOM	1312	CB	ASP	165	9.809	6.009	68.764	1.00	43.20
ATOM	1313	CG	ASP	165	8.627	6.038	67.838	1.00	43.20
ATOM	1314	OD1	ASP	165	7.598	5.410	68.157	1.00	43.20
ATOM	1315	OD2	ASP	165	8.733	6.683	66.781	1.00	43.20
ATOM	1316	C	ASP	165	10.669	5.957	71.081	1.00	36.74
ATOM	1317	O	ASP	165	11.175	4.910	71.468	1.00	36.74

	ATOM	1318	N	GLU	166	11.180	7.148	71.360	1.00	35.71
	ATOM	1319	CA	GLU	166	12.379	7.271	72.159	1.00	35.71
	ATOM	1320	CB	GLU	166	12.782	8.744	72.247	1.00	54.57
	ATOM	1321	CG	GLU	166	13.811	9.057	73.318	1.00	54.57
	ATOM	1322	CD	GLU	166	14.165	10.542	73.381	1.00	54.57
	ATOM	1323	OE1	GLU	166	14.607	11.010	74.458	1.00	54.57
	ATOM	1324	OE2	GLU	166	14.010	11.233	72.346	1.00	54.57
	ATOM	1325	C	GLU	166	12.131	6.678	73.549	1.00	35.71
	ATOM	1326	O	GLU	166	12.978	5.958	74.083	1.00	35.71
	ATOM	1327	N	PHE	167	10.966	6.957	74.128	1.00	32.84
	ATOM	1328	CA	PHE	167	10.664	6.437	75.455	1.00	32.84
	ATOM	1329	CB	PHE	167	9.675	7.349	76.181	1.00	33.04
	ATOM	1330	CG	PHE	167	10.337	8.524	76.824	1.00	33.04
	ATOM	1331	CD1	PHE	167	10.602	9.677	76.093	1.00	33.04
	ATOM	1332	CD2	PHE	167	10.806	8.435	78.127	1.00	33.04
	ATOM	1333	CE1	PHE	167	11.330	10.732	76.650	1.00	33.04
	ATOM	1334	CE2	PHE	167	11.536	9.483	78.695	1.00	33.04
	ATOM	1335	CZ	PHE	167	11.802	10.633	77.949	1.00	33.04
	ATOM	1336	C	PHE	167	10.205	4.992	75.492	1.00	32.84
	ATOM	1337	O	PHE	167	10.456	4.295	76.471	1.00	32.84
	ATOM	1338	N	ILE	168	9.534	4.536	74.439	1.00	29.66
	ATOM	1339	CA	ILE	168	9.129	3.141	74.378	1.00	29.66
	ATOM	1340	CB	ILE	168	8.321	2.835	73.090	1.00	23.21
	ATOM	1341	CG2	ILE	168	8.154	1.336	72.914	1.00	23.21

	ATOM	1342	CG1	ILE	168	6.956	3.527	73.151	1.00	23.21
	ATOM	1343	CD1	ILE	168	6.045	3.006	74.261	1.00	23.21
	ATOM	1344	C	ILE	168	10.441	2.357	74.333	1.00	29.66
	ATOM	1345	O	ILE	168	10.576	1.314	74.963	1.00	29.66
	ATOM	1346	N	GLU	169	11.409	2.876	73.584	1.00	31.65
	ATOM	1347	CA	GLU	169	12.714	2.233	73.460	1.00	31.65
	ATOM	1348	CB	GLU	169	13.622	3.015	72.512	1.00	93.52
	ATOM	1349	CG	GLU	169	13.972	2.279	71.237	1.00	93.52
	ATOM	1350	CD	GLU	169	15.263	2.784	70.617	1.00	93.52
	ATOM	1351	OE1	GLU	169	16.259	2.029	70.623	1.00	93.52
	ATOM	1352	OE2	GLU	169	15.287	3.936	70.133	1.00	93.52
	ATOM	1353	C	GLU	169	13.399	2.133	74.811	1.00	31.65
	ATOM	1354	O	GLU	169	13.927	1.084	75.166	1.00	31.65
	ATOM	1355	N	LYS	170	13.397	3.233	75.557	1.00	29.27
	ATOM	1356	CA	LYS	170	14.020	3.262	76.869	1.00	29.27
	ATOM	1357	CB	LYS	170	13.933	4.665	77.479	1.00	37.44
	ATOM	1358	CG	LYS	170	14.604	5.778	76.681	1.00	37.44
	ATOM	1359	CD	LYS	170	14.878	6.964	77.592	1.00	37.44
	ATOM	1360	CE	LYS	170	15.005	8.291	76.849	1.00	37.44
	ATOM	1361	NZ	LYS	170	16.177	8.363	75.931	1.00	37.44
	ATOM	1362	C	LYS	170	13.345	2.258	77.799	1.00	29.27
	ATOM	1363	O	LYS	170	13.999	1.647	78.646	1.00	29.27
	ATOM	1364	N	LEU	171	12.034	2.090	77.651	1.00	41.19
	ATOM	1365	CA	LEU	171	11.309	1.134	78.481	1.00	41.19

	ATOM	1366	CB	LEU	171	9.802	1.224	78.237	1.00	27.02
	ATOM	1367	CG	LEU	171	8.903	1.952	79.251	1.00	27.02
	ATOM	1368	CD1	LEU	171	9.643	2.164	80.555	1.00	27.02
	ATOM	1369	CD2	LEU	171	8.446	3.275	78.696	1.00	27.02
	ATOM	1370	C	LEU	171	11.789	-0.271	78.153	1.00	41.19
	ATOM	1371	O	LEU	171	12.092	-1.059	79.048	1.00	41.19
	ATOM	1372	N	ASP	172	11.872	-0.577	76.863	1.00	35.05
	ATOM	1373	CA	ASP	172	12.321	-1.890	76.435	1.00	35.05
	ATOM	1374	CB	ASP	172	12.324	-2.001	74.907	1.00	41.75
	ATOM	1375	CG	ASP	172	10.923	-2.075	74.324	1.00	41.75
	ATOM	1376	OD1	ASP	172	10.790	-2.135	73.080	1.00	41.75
	ATOM	1377	OD2	ASP	172	9.954	-2.077	75.111	1.00	41.75
	ATOM	1378	C	ASP	172	13.711	-2.152	76.962	1.00	35.05
	ATOM	1379	O	ASP	172	14.037	-3.283	77.336	1.00	35.05
	ATOM	1380	N	GLU	173	14.533	-1.110	77.003	1.00	32.93
	ATOM	1381	CA	GLU	173	15.892	-1.278	77.491	1.00	32.93
	ATOM	1382	CB	GLU	173	16.706	-0.007	77.306	1.00	41.86
	ATOM	1383	CG	GLU	173	18.142	-0.213	77.734	1.00	41.86
	ATOM	1384	CD	GLU	173	18.999	1.008	77.563	1.00	41.86
	ATOM	1385	OE1	GLU	173	18.671	1.847	76.688	1.00	41.86
	ATOM	1386	OE2	GLU	173	20.009	1.112	78.294	1.00	41.86
	ATOM	1387	C	GLU	173	15.873	-1.630	78.965	1.00	32.93
	ATOM	1388	O	GLU	173	16.495	-2.601	79.400	1.00	32.93
	ATOM	1389	N	VAL	174	15.160	-0.811	79.726	1.00	31.38

	ATOM	1390	CA	VAL	174	15.023	-0.990	81.156	1.00	31.38
	ATOM	1391	CB	VAL	174	14.087	0.108	81.715	1.00	34.37
	ATOM	1392	CG1	VAL	174	13.572	-0.277	83.053	1.00	34.37
	ATOM	1393	CG2	VAL	174	14.846	1.426	81.815	1.00	34.37
	ATOM	1394	C	VAL	174	14.506	-2.401	81.488	1.00	31.38
	ATOM	1395	O	VAL	174	14.896	-2.997	82.492	1.00	31.38
	ATOM	1396	N	PHE	175	13.631	-2.943	80.648	1.00	32.64
	ATOM	1397	CA	PHE	175	13.136	-4.290	80.895	1.00	32.64
	ATOM	1398	CB	PHE	175	11.999	-4.661	79.947	1.00	30.70
	ATOM	1399	CG	PHE	175	11.718	-6.133	79.920	1.00	30.70
	ATOM	1400	CD1	PHE	175	11.187	-6.770	81.038	1.00	30.70
	ATOM	1401	CD2	PHE	175	12.056	-6.898	78.810	1.00	30.70
	ATOM	1402	CE1	PHE	175	11.001	-8.159	81.056	1.00	30.70
	ATOM	1403	CE2	PHE	175	11.878	-8.280	78.811	1.00	30.70
	ATOM	1404	CZ	PHE	175	11.348	-8.916	79.938	1.00	30.70
	ATOM	1405	C	PHE	175	14.262	-5.296	80.695	1.00	32.64
	ATOM	1406	O	PHE	175	14.444	-6.196	81.509	1.00	32.64
	ATOM	1407	N	GLU	176	15.002	-5.150	79.597	1.00	36.36
	ATOM	1408	CA	GLU	176	16.120	-6.039	79.290	1.00	36.36
	ATOM	1409	CB	GLU	176	16.826	-5.595	78.011	1.00	49.35
	ATOM	1410	CG	GLU	176	16.862	-6.649	76.921	1.00	49.35
	ATOM	1411	CD	GLU	176	17.554	-7.935	77.348	1.00	49.35
	ATOM	1412	OE1	GLU	176	18.722	-7.869	77.793	1.00	49.35
	ATOM	1413	OE2	GLU	176	16.929	-9.015	77.232	1.00	49.35

ATOM	1414	C	GLU	176	17.125	-6.050	80.428	1.00	36.36
ATOM	1415	O	GLU	176	17.603	-7.110	80.832	1.00	36.36
ATOM	1416	N	ILE	177	17.444	-4.866	80.942	1.00	35.83
ATOM	1417	CA	ILE	177	18.398	-4.740	82.033	1.00	35.83
ATOM	1418	CB	ILE	177	18.606	-3.259	82.422	1.00	29.26
ATOM	1419	CG2	ILE	177	19.370	-3.163	83.737	1.00	29.26
ATOM	1420	CG1	ILE	177	19.358	-2.525	81.303	1.00	29.26
ATOM	1421	CD1	ILE	177	20.851	-2.863	81.233	1.00	29.26
ATOM	1422	C	ILE	177	17.936	-5.513	83.265	1.00	35.83
ATOM	1423	O	ILE	177	18.738	-6.162	83.946	1.00	35.83
ATOM	1424	N	LYS	178	16.643	-5.448	83.554	1.00	34.13
ATOM	1425	CA	LYS	178	16.112	-6.147	84.707	1.00	34.13
ATOM	1426	CB	LYS	178	14.687	-5.684	85.003	1.00	28.12
ATOM	1427	CG	LYS	178	14.188	-6.109	86.376	1.00	28.12
ATOM	1428	CD	LYS	178	15.059	-5.482	87.469	1.00	28.12
ATOM	1429	CE	LYS	178	14.588	-5.848	88.857	1.00	28.12
ATOM	1430	NZ	LYS	178	15.375	-5.118	89.878	1.00	28.12
ATOM	1431	C	LYS	178	16.117	-7.645	84.444	1.00	34.13
ATOM	1432	O	LYS	178	16.470	-8.440	85.325	1.00	34.13
ATOM	1433	N	LYS	179	15.719	-8.028	83.232	1.00	34.54
ATOM	1434	CA	LYS	179	15.682	-9.435	82.865	1.00	34.54
ATOM	1435	CB	LYS	179	15.233	-9.610	81.419	1.00	32.56
ATOM	1436	CG	LYS	179	15.201	-11.056	80.963	1.00	32.56
ATOM	1437	CD	LYS	179	14.889	-11.124	79.487	1.00	32.56

ATOM	1438	CE	LYS	179	14.908	-12.551	78.949	1.00	32.56
ATOM	1439	NZ	LYS	179	14.654	-12.572	77.478	1.00	32.56
ATOM	1440	C	LYS	179	17.064	-10.035	83.044	1.00	34.54
ATOM	1441	O	LYS	179	17.202	-11.146	83.554	1.00	34.54
ATOM	1442	N	GLU	180	18.085	-9.297	82.623	1.00	32.37
ATOM	1443	CA	GLU	180	19.455	-9.765	82.765	1.00	32.37
ATOM	1444	CB	GLU	180	20.427	-8.792	82.106	1.00	44.31
ATOM	1445	CG	GLU	180	20.288	-8.756	80.608	1.00	44.31
ATOM	1446	CD	GLU	180	21.035	-7.609	79.980	1.00	44.31
ATOM	1447	OE1	GLU	180	20.809	-7.366	78.779	1.00	44.31
ATOM	1448	OE2	GLU	180	21.841	-6.951	80.677	1.00	44.31
ATOM	1449	C	GLU	180	19.793	-9.908	84.232	1.00	32.37
ATOM	1450	O	GLU	180	20.371	-10.898	84.635	1.00	32.37
ATOM	1451	N	GLU	181	19.422	-8.920	85.035	1.00	35.90
ATOM	1452	CA	GLU	181	19.708	-8.966	86.465	1.00	35.90
ATOM	1453	CB	GLU	181	19.124	-7.738	87.160	1.00	47.46
ATOM	1454	CG	GLU	181	19.444	-7.662	88.642	1.00	47.46
ATOM	1455	CD	GLU	181	18.738	-6.511	89.342	1.00	47.46
ATOM	1456	OE1	GLU	181	17.501	-6.522	89.412	1.00	47.46
ATOM	1457	OE2	GLU	181	19.419	-5.589	89.823	1.00	47.46
ATOM	1458	C	GLU	181	19.125	-10.230	87.096	1.00	35.90
ATOM	1459	O	GLU	181	19.771	-10.892	87.910	1.00	35.90
ATOM	1460	N	ILE	182	17.899	-10.555	86.709	1.00	38.32
ATOM	1461	CA	ILE	182	17.210	-11.717	87.243	1.00	38.32

	ATOM	1462	CB	ILE	182	15.724	-11.673	86.870	1.00	31.34
	ATOM	1463	CG2	ILE	182	15.056	-13.010	87.194	1.00	31.34
	ATOM	1464	CG1	ILE	182	15.051	-10.513	87.595	1.00	31.34
	ATOM	1465	CD1	ILE	182	13.680	-10.173	87.047	1.00	31.34
	ATOM	1466	C	ILE	182	17.798	-13.040	86.773	1.00	38.32
	ATOM	1467	O	ILE	182	17.841	-13.997	87.541	1.00	38.32
	ATOM	1468	N	MET	183	18.249	-13.094	85.520	1.00	47.57
	ATOM	1469	CA	MET	183	18.819	-14.318	84.957	1.00	47.57
	ATOM	1470	CB	MET	183	18.614	-14.370	83.444	1.00	45.73
	ATOM	1471	CG	MET	183	17.174	-14.221	82.994	1.00	45.73
	ATOM	1472	SD	MET	183	16.076	-15.382	83.795	1.00	45.73
	ATOM	1473	CE	MET	183	16.837	-16.936	83.323	1.00	45.73
	ATOM	1474	C	MET	183	20.299	-14.434	85.261	1.00	47.57
	ATOM	1475	O	MET	183	20.777	-15.516	85.583	1.00	47.57
	ATOM	1476	N	GLU	184	21.026	-13.325	85.128	1.00	64.62
	ATOM	1477	CA	GLU	184	22.455	-13.295	85.437	1.00	64.62
	ATOM	1478	CB	GLU	184	23.104	-12.016	84.885	1.00	100.23
	ATOM	1479	CG	GLU	184	22.781	-11.669	83.422	1.00	100.23
	ATOM	1480	CD	GLU	184	23.213	-12.733	82.429	1.00	100.23
	ATOM	1481	OE1	GLU	184	24.282	-13.344	82.642	1.00	100.23
	ATOM	1482	OE2	GLU	184	22.490	-12.945	81.426	1.00	100.23
	ATOM	1483	C	GLU	184	22.528	-13.313	86.974	1.00	64.62
	ATOM	1484	O	GLU	184	23.295	-12.582	87.596	1.00	64.62
	ATOM	1485	N	PHE	185	21.677	-14.170	87.538	1.00	64.82

ATOM	1486	CA	PHE	185	21.470	-14.427	88.968	1.00	64.82
ATOM	1487	CB	PHE	185	21.845	-15.885	89.308	1.00	100.63
ATOM	1488	CG	PHE	185	23.303	-16.226	89.133	1.00	100.63
ATOM	1489	CD1	PHE	185	24.222	-15.967	90.146	1.00	100.63
ATOM	1490	CD2	PHE	185	23.744	-16.877	87.984	1.00	100.63
ATOM	1491	CE1	PHE	185	25.554	-16.363	90.018	1.00	100.63
ATOM	1492	CE2	PHE	185	25.074	-17.272	87.854	1.00	100.63
ATOM	1493	CZ	PHE	185	25.975	-17.015	88.872	1.00	100.63
ATOM	1494	C	PHE	185	22.019	-13.492	90.040	1.00	64.82
ATOM	1495	O	PHE	185	21.202	-13.108	90.910	1.00	64.82
ATOM	1496	OT	PHE	185	23.222	-13.161	90.023	1.00	100.63
ATOM	1497	OH2	WAT	1	7.314	-7.392	118.599	1.00	28.51
ATOM	1498	OH2	WAT	2	20.141	-10.167	116.646	1.00	41.71
ATOM	1499	OH2	WAT	3	-0.839	7.103	71.695	1.00	38.40
ATOM	1500	OH2	WAT	4	20.724	-12.318	113.141	1.00	36.06
ATOM	1501	OH2	WAT	5	13.214	7.193	109.995	1.00	34.42
ATOM	1502	OH2	WAT	6	-4.563	25.067	61.299	1.00	35.61
ATOM	1503	OH2	WAT	7	9.162	-10.160	92.783	1.00	40.02
ATOM	1504	OH2	WAT	8	15.821	7.078	82.761	1.00	45.31
ATOM	1505	OH2	WAT	9	15.568	0.183	88.102	1.00	24.68
ATOM	1506	OH2	WAT	10	17.031	-3.108	93.557	1.00	33.93
ATOM	1507	OH2	WAT	11	-5.066	12.003	70.605	1.00	31.32
ATOM	1508	OH2	WAT	12	17.672	-16.020	114.048	1.00	36.87
ATOM	1509	OH2	WAT	13	7.862	-1.817	71.942	1.00	33.70

ATOM	1510	OH2	WAT	14	8.138	-13.701	94.980	1.00	33.33
ATOM	1511	OH2	WAT	15	11.279	0.783	115.697	1.00	32.56
ATOM	1512	OH2	WAT	16	16.003	6.468	88.212	1.00	29.59
ATOM	1513	OH2	WAT	17	8.553	-16.970	109.277	1.00	43.42
ATOM	1514	OH2	WAT	18	18.461	-2.485	119.281	1.00	42.15
ATOM	1515	OH2	WAT	19	6.746	-17.081	107.102	1.00	37.19
ATOM	1516	OH2	WAT	20	2.389	-1.792	87.493	1.00	33.97
ATOM	1517	OH2	WAT	21	16.366	-2.230	89.109	1.00	26.69
ATOM	1518	OH2	WAT	22	5.158	-12.795	87.845	1.00	43.81
ATOM	1519	OH2	WAT	23	5.761	7.139	104.779	1.00	36.64
ATOM	1520	OH2	WAT	24	10.078	-21.141	83.981	1.00	45.96
ATOM	1521	OH2	WAT	25	1.702	29.020	57.574	1.00	39.21
ATOM	1522	OH2	WAT	26	21.863	-2.142	99.878	1.00	44.34
ATOM	1523	OH2	WAT	27	17.198	13.784	85.530	1.00	51.52
ATOM	1524	OH2	WAT	28	-0.400	2.402	82.821	1.00	35.70
ATOM	1525	OH2	WAT	29	13.686	5.872	89.473	1.00	44.84
ATOM	1526	OH2	WAT	30	17.457	-13.476	113.108	1.00	33.62
ATOM	1527	OH2	WAT	31	16.228	-0.207	73.422	1.00	40.99
ATOM	1528	OH2	WAT	32	19.350	1.763	107.228	1.00	41.09
ATOM	1529	OH2	WAT	33	21.908	-12.207	93.466	1.00	47.34
ATOM	1530	OH2	WAT	34	2.605	-3.562	103.490	1.00	38.48
ATOM	1531	OH2	WAT	35	-2.900	25.786	57.810	1.00	32.08
ATOM	1532	OH2	WAT	36	9.098	-15.151	82.349	1.00	38.27
ATOM	1533	OH2	WAT	37	-12.293	25.412	66.878	1.00	41.13

ATOM	1534	OH2	WAT	38	15.500	-8.451	95.623	1.00	36.30
ATOM	1535	OH2	WAT	39	-2.144	0.572	109.124	1.00	41.18
ATOM	1536	OH2	WAT	40	1.366	0.844	117.806	1.00	43.55
ATOM	1537	OH2	WAT	41	-3.862	8.488	66.607	1.00	42.64
ATOM	1538	OH2	WAT	42	14.848	-25.238	90.334	1.00	44.95
ATOM	1539	OH2	WAT	43	21.959	-4.948	118.899	1.00	44.58
ATOM	1540	OH2	WAT	44	8.447	-16.493	95.999	1.00	57.34
ATOM	1541	OH2	WAT	45	-3.320	18.594	80.730	1.00	44.65
ATOM	1542	OH2	WAT	46	4.042	3.465	70.117	1.00	42.29
ATOM	1543	OH2	WAT	47	0.370	-3.250	110.892	1.00	34.03
ATOM	1544	OH2	WAT	48	1.694	-13.510	110.447	1.00	43.12
ATOM	1545	OH2	WAT	49	16.216	-2.085	84.867	1.00	29.17
ATOM	1546	OH2	WAT	50	15.797	-7.322	122.289	1.00	49.41
ATOM	1547	OH2	WAT	51	18.922	-12.474	79.878	1.00	42.31
ATOM	1548	OH2	WAT	52	-5.107	22.838	73.181	1.00	38.51
ATOM	1549	OH2	WAT	53	14.563	4.864	98.821	1.00	32.28
ATOM	1550	OH2	WAT	54	13.994	-16.023	105.563	1.00	44.24
ATOM	1551	OH2	WAT	55	-4.133	13.720	66.033	1.00	53.29
ATOM	1552	OH2	WAT	56	10.183	28.544	75.646	1.00	56.33
ATOM	1553	OH2	WAT	57	-3.774	-9.836	113.284	1.00	59.77
ATOM	1554	OH2	WAT	58	17.629	0.775	96.137	1.00	37.95
ATOM	1555	OH2	WAT	59	6.043	1.046	121.396	1.00	35.94
ATOM	1556	OH2	WAT	60	4.946	-12.576	116.234	1.00	49.56
ATOM	1557	OH2	WAT	61	-4.890	3.540	80.417	1.00	46.86

ATOM	1558	OH2	WAT	62	-1.025	-13.655	106.259	1.00	39.99
ATOM	1559	OH2	WAT	63	10.494	2.348	70.136	1.00	40.25
ATOM	1560	OH2	WAT	64	0.561	-14.185	101.707	1.00	47.94
ATOM	1561	OH2	WAT	65	4.913	-11.710	91.331	1.00	52.16
ATOM	1562	OH2	WAT	66	3.448	29.483	61.850	1.00	33.98
ATOM	1563	OH2	WAT	67	2.424	5.726	69.262	1.00	57.07
ATOM	1564	OH2	WAT	68	24.893	-19.561	96.089	1.00	55.67
ATOM	1565	OH2	WAT	69	-0.538	31.270	63.339	1.00	29.89
ATOM	1566	OH2	WAT	70	-4.671	6.956	69.710	1.00	49.13
ATOM	1567	OH2	WAT	71	16.579	2.427	107.056	1.00	41.13
ATOM	1568	OH2	WAT	72	16.449	-0.978	120.834	1.00	51.89
ATOM	1569	OH2	WAT	73	3.860	-5.877	90.214	1.00	44.03